

Access DB#

47046

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

## STAFF USE ONLY

Searcher: D. Schreiber  
Searcher Phone #: 308-4292  
Searcher Location: CM1 12E18  
Date Searcher Picked Up: 7/23  
Date Completed: 7/23  
Searcher Prep & Review Time: 7  
Final Prep Time: \_\_\_\_\_  
Total Time: 15

## Type of Search

NA Sequence (#) \_\_\_\_\_  
AA Sequence (#) 4  
Structure (#) \_\_\_\_\_  
Bibliographic \_\_\_\_\_  
Litigation \_\_\_\_\_  
Fulltext \_\_\_\_\_  
Patent Family \_\_\_\_\_  
Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_  
Dialog \_\_\_\_\_  
Questel/Orbit \_\_\_\_\_  
Dr Link \_\_\_\_\_  
Lexis/Nexis \_\_\_\_\_  
Sequence Systems CompuGen Ig & FastDB  
WWW/Internet \_\_\_\_\_  
Other (specify) \_\_\_\_\_

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K19155 Fin 47046

From: Zeman, Mary  
 Sent: Wednesday, July 18, 2001 10:49 AM  
 To: STIC-Biotech/ChemLib  
 Subject: SEQ Search. 09/636801

CRFE  
ALL

Please search SEQ ID NO: 392 in all files but not pending files.

Please search SEQ ID NO: 392 against the following parent files (For priority):  
 09/617747; 09/404879; 09/338933; 09/216003 and 09/215681

Paper printout please

Thank you

Mary Zeman

Examiner, 1631

Office 12A17

Mailbox 12D01

Elected Gpl clms  
 1, 2, 9-12, 21, 23, 24 + 69-72  
 SEQ ID NO 392 paper #9  
 7/6/01  
 No args.

NUCLEO SEQ 391 "provide full length sequences incorporating certain", p53

392 Not in Table @ p50-53 proteins encoded by OSE

No protein in '003 + 68

p53 = OSE  
 seq 392 = "b" form

OSE polyclonal Ab p54  
 used 20-mers of OSE

1/6 ovarian tissue samples was positive for OSE p55  
 No controls

p56 FACS sorting - what kind of cells?  
 Breast cancer HEK293  
 Not MB415? or

1/55  
 10/16/00

clms 9-12  
 vaccine

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 11.22 Seconds

(without alignments)  
943,400 Million cell updates/sec

Title: US-09-636-801-392

1574

Sequence: 1 HASAHASGROQLHSASTQI.....SSFAISWALLPLSPYIMLK 309

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215.5	13.7	526	1	BUTY_BOVIN
2	211.5	13.4	526	1	BUTY_HUMAN
3	178.5	11.3	524	1	BUTY_MOUSE
4	163.5	10.4	299	1	CD80_RABBIT
5	152	9.7	245	1	MOG_RAT
6	150.5	9.6	329	1	MOG_MOUSE
7	147.5	9.4	329	1	CD86_HUMAN
8	147.5	9.4	330	1	CD86_RABBIT
9	147.5	9.4	558	1	Y653_HUMAN
10	144	9.1	247	1	MOG_HUMAN
11	143.5	9.1	309	1	CD86_MOUSE
12	140.5	8.9	246	1	MOG_BOVIN
13	135	8.6	761	1	NCA2_HUMAN
14	135	8.6	848	1	NCA1_HUMAN
15	132.5	8.4	853	1	NCA1_BOVIN
16	131	8.3	1091	1	NCA1_CHICK
17	130.5	8.3	725	1	NCA2_MOUSE
18	130.5	8.3	1115	1	NCA1_MOUSE
19	128.5	8.2	858	1	NCA1_RAT
20	126.5	8.0	1088	1	NCA1_MOUSE
21	125.5	8.0	298	1	VEJA_HUMAN
22	124	7.9	306	1	CD80_MOUSE
23	123	7.8	365	1	CD80_MOUSE
24	121	7.7	1010	1	CD80_MOUSE
25	120	7.6	215	1	CD82_RAT
26	120	7.6	288	1	CD80_HUMAN
27	120	7.6	333	1	AMAL_DROME
28	120	7.6	365	1	CD80_HUMAN
29	119	7.6	323	1	CD80_HUMAN
30	115.5	7.3	1092	1	NCA2_XENLA
31	113.5	7.2	1336	1	VEJA_HUMAN
32	113.5	7.2	1461	1	NEO1_HUMAN
33	113	7.2	359	1	LACH_DROME

## ALIGNMENTS

RESULT	1	STANDARD	PRT	526 AA.
ID	BUTY_BOVIN			
AC	P18892; O18955; O18959;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	BUTYRHOPIHILIN PRECURSOR (BT).			
GN	BTN.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.			
RX	MEDLINE=90354441; PubMed=2387867;			
RA	Jack L.J.W., Mather I.H.;			
RT	"Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein expressed in mammary tissue and secreted in association with the milk-fat globule membrane during lactation.";			
RT	J. Biol. Chem. 265:14481-14486(1990).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-HOLSTEIN-FRIESIAN;			
RC	Daye H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,			
RA	Mather I.H., Wilkins R.V.;			
RT	Submitted (May-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RA	Seyfert H., Luethen F.;			
RT	Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	CARBOHYDRATE-LINKAGE SITES.			
RX	MEDLINE=95293916; PubMed=7775382;			
RA	Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;			
RT	"Site-specific glycosylation of bovine butyrophilin.";			
RT	J. Biochem. 117:147-157(1995).			
RL	[5]			
RP	FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA MEMBRANE.			
CC	- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.			
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.			
CC	- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			

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DR EMBL; M35551; AAB39766.1; -  
DR EMBL; AF005497; AAB62889.1; -  
DR EMBL; Z93323; CAB07533.1; -  
DR PIR; A37821; A37821.  
DR InterPro; IPR00107; -  
DR InterPro; IPR003006; -  
DR Pfam; PF00622; SPRY; 1.  
DR Pfam; PF00047; 1g; 1.  
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.  
FT SIGNAL 1 26  
FT CHAIN 1 26  
FT DOMAIN 27 526  
FT TRANSMEM 27 242  
FT DOMAIN 243 269  
FT DOMAIN 270 526  
FT CARBOHD 55 526  
FT CARBOHD 215 215  
FT CONFLICT 35 35  
FT CONFLICT 230 230  
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 13.7%; Score 215.5; DB 1; Length 526;  
Best Local Similarity 24.5%; Pred. No. 3.8e-10;  
Matches 48; Conservative 49; Mismatches 94; Indels 5; Gaps 4;

QY 75 IGEDGILCTFEPPDKILSDIYQWLKEGVLGVHFEKCKDLSRDEMRGRATVAFDQ 134  
Db 42 VGEDDELPCRLSPNVAHAKMELRERKVPVAVSREGQEGEGEMAEYRGRVSLVEDH 101  
QY 135 VVGNASRLKKNVQLTDAGTYKCYIITSKGNANLEVTGAF-SMEYNAVVDYNASSE-T 192  
Db 102 IAGSEVAVRIGVAKSDGEGYCFRQDENEALYHLKVALGSDPHSMQVQSGELQ 161  
QY 193 LRCEAPRPFQPTVYVASOVDOGANFSEVSNFSPELSENVTMKVSVLYNTINNTYSC 252  
Db 162 LECTSGVWPEPQVOM--RTHRGEEFSPKSESRNPDEGLFTVAVSVIIRDSMKNV-SC 218  
QY 253 MIENDIAKATGIRKYT 268  
Db 219 CIRNLLGOEKEVEVS 234

RESULT 2  
BUTY\_HUMAN STANDARD; PRT; 526 AA.  
AC Q13410;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE BUTYROPHILIN PRECURSOR (BT).  
GN BTN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast;  
RX MEDLINE=96201696; PubMed=8611614;  
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;  
RT "Cloning and sequence analysis of human butyrophilin reveals a  
RT potential receptor function."  
RL Blochm. Biophys. Acta 1306:1-4(1996).  
CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT  
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE  
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA  
CC MEMBRANE (BY SIMILARITY).  
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE  
CC (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.  
CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).  
CC  
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DR EMBL; U39576; AAC50489.1; -  
DR MIM; 601610; -  
DR InterPro; IPR00107; -  
DR InterPro; IPR003006; -  
DR Pfam; PF00622; SPRY; 1.  
DR Pfam; PF00047; 1g; 1.  
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.  
FT SIGNAL 1 26  
FT CHAIN 1 26  
FT DOMAIN 27 526  
FT TRANSMEM 27 242  
FT DOMAIN 243 269  
FT CARBOHD 55 526  
FT CARBOHD 215 215  
SQ SEQUENCE 526 AA; 59004 MW; E9EACACFBDAF94D5 CRC64;

Query Match 13.4%; Score 211.5; DB 1; Length 526;  
Best Local Similarity 26.6%; Pred. No. 8.1e-10;  
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILCTFEPPDKILSDIYQWLKEGVLGVHFEKCKDLSRDEMRGRATVAFDQ 134  
Db 42 VGEDDELPCRLSPNVAHAKMELRERKVPVAVSREGQEGEGEMAEYRGRVSLVEDH 101  
QY 135 VVGNASRLKKNVQLTDAGTYKCYIITSKGNANLEVTGAF-SMEYNAVVDYNASSE-T 192  
Db 102 IAKGRVALRIRGVASDGEYCFRQDENEALYHLKVALGSDPHSMQVQSGELQ 161  
QY 193 LRCEAPRPFQPTVYVASOVDOGANFSEVSNFSPELSENVTMKVSVLYNTINNTYSC 252  
Db 162 LECTSGVWPEPQVOM--RTSKGEKFPSTSE-SRNPDEGLFTVAVSVIIRDTSPKNSC 218  
QY 253 MIEN 256  
Db 219 YLON 222

RESULT 3  
BUTY\_MOUSE STANDARD; PRT; 524 AA.  
AC Q62556; P97392;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE BUTYROPHILIN PRECURSOR (BT).  
GN BTN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Mammary gland;  
RX MEDLINE=97148936; PubMed=8995761;  
RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;  
RT "Structural organization and mammary-specific expression of the  
RT butyrophilin gene."  
RL Mamm. Genome 7:900-905(1996).  
RN [2]



A:Molecule type: mRNA  
A:Residues: 1-526 <TAV>  
A:Cross-references: EMBL:U039576; NID:g1326082; PIDN:AAC50489.1; PID:g1326083

Query Match 13.4%; Score 211.5; DB 2; Length 526;  
Best Local Similarity 26.6%; Pred. No. 1.4e-08;  
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILSCFEPDIKLSIDIVIQWLKEGVLGVHEFEKSKDELSEODEMFRGRTRAVFADQ 134  
DB 42 VEDDELPELRLEPNSAEHLERLFRKKVSPAVLVHRDREDAEQMPYRGRATLVQDG 101  
QY 135 VIVGNASRLKKNVQLTDAGTYKCIITTSKGNANLEYKTGAF-SMPEVNVDMASSE-T 192  
DB 102 IAKGRALAIRGVRSVSDDEYTCFREDGSEYEAALVHLKVAALGSDPHISMVQENGECIC 161  
QY 193 LRCEAPRMPQPTVWASQVDGANESEVSNFSFELSENVTMKVSVLVYNTINNTYSC 252  
DB 162 LRCTSGWYPEPOVOW--RTSKGEKFPSTSE-SRNPDEGLFTVAASVITIRDTSTKNVSC 218  
QY 253 MIEN 256  
DB 219 YIQN 222

RESULT 3  
S65133  
butyrophillin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C:Accession: S65133  
R:Ishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.  
Biochim. Biophys. Acta 1245, 285-292, 1995  
A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophillin specifically associated  
A:Reference number: S65133; MUID:96125722  
A:Accession: S65133  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-487 <ISH>  
A:Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; PID:g1246079

Query Match 10.9%; Score 171.5; DB 2; Length 487;  
Best Local Similarity 22.4%; Pred. No. 1.4e-05;  
Matches 44; Conservative 51; Mismatches 92; Indels 9; Gaps 4;

QY 77 EDCILSCFEPPIKLSIDIVIQWLKEGVLGVHEFEKSKDELSEODEMFRGRTRAVFADQYI 136  
DB 8 DDAELTCGSPNASSEYEMELMFROTSTAVLLYRDGQEQGQMTREKGRATLTATAGLL 67  
QY 137 VGNASRLKKNVQLTDAGTYKCIITTSKGNANLEYKTGAF-SMPEVNVDMASSE-TLR 194  
DB 68 DGRATLLLRDVAFSDQGERCLFKDNDDFEAAVILKVAAVSSDQISMTVQENGEMELE 127  
QY 195 CEAPRMPQPTVWASQVDGANESEVSNFSFELSENVTMKVSVLVYNTINNTYSC 252  
DB 128 CTSWGWYPEPOVOWMT-----GNREMLPSTDSKKNHEGLFTVAVSMWISDSIKNSC 182  
QY 253 MIENDIAKATGDIKYT 268  
DB 183 CTQNTLLGGCKEVEIS 198

RESULT 4  
T09058  
butyrophillin homolog - mouse (fragment)  
N:Alternate names: butyrophillin-like protein  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C:Accession: T09058  
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Se  
submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.  
A:Reference number: Z16543  
A:Accession: T09058  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-391 <ROW>  
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564946  
A:Note: BAC 29N7  
C:Genetics:  
A:Map position: 17  
A:Note: butyrophillin-like  
A:Note: Intron positions not resolved (incomplete sequence)

Query Match 10.7%; Score 168.5; DB 2; Length 391;  
Best Local Similarity 26.3%; Pred. No. 1.9e-05;  
Matches 52; Conservative 45; Mismatches 82; Indels 19; Gaps 8;

QY 76 GEDGILSCFEPDIKLSI-VIQWLKEGVLGVHEFEKSKDELSEODEMFRGRTRAVFADQ 134  
DB 26 GREALIPCSVIVPMVNEEELRWYRNRPFAVLVYRDQEQKRDQMEYSWRTSLVKDQ 85  
QY 135 VIVGNASRLKKNVQLTDAGTYKCIITTSKGNANLEYKTGAF-SMPEVNV-DYASSFT 192  
DB 86 FHQGTAAVRITQNIQASDSICVCHFRMGQFHEALTELKVAAMGSVEVHIGPEDGVC 145  
QY 193 LRCEAPRMPQPTVWASQVDGANESEVSNFSFELSENVT-----TMKVY--SVLYN 243  
DB 146 VVCMNTSGWYPEPOVHMRD--SRGEKFT----ASLEHGDADAGLTRTERSLVYRROSSVKN 199  
QY 244 VTINNTYSCMIENDIAKA 261  
DB 200 V-ICSTFNSILGEEKAMA 216

RESULT 5  
I46690  
CD80 precursor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 29-Sep-1999  
C:Accession: I46690  
R:Isono, T.; Seto, A.  
Immunogenetics 42, 217-220, 1995  
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole  
A:Reference number: I46689; MUID:95369849  
A:Accession: I46690  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-299 <ISO>  
A:Cross-references: GB:D49843; NID:g755096; PIDN:BA008643.1; PID:g755097  
C:Superfamily: B-Lymphocyte restricted antigen B7

Query Match 10.4%; Score 163.5; DB 2; Length 299;  
Best Local Similarity 25.3%; Pred. No. 3.2e-05;  
Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISITILGAILILGFGISGRHSITVTVAAGNIGEDGILSCFEPDI-KLSDIVIQW 98  
DB 19 LCLLALAC---LHSSSGIS-----QVTK-----SVKEAALSCDYNSIDELAKRIYW 65  
QY 99 LKEG--VIGLVHEFEKSKDELSEODEMFRGRTRAVFADQYVGNASRLKKNVQLTDAGTYK 156  
DB 66 OKDQGVLSII-----SGQVEWPE--YKNRT--PPD--IINNLSIMILALRLSDKGYT 114  
QY 157 CYITTSKGNANLEYKTGA-----SMPEV-----NDVYASSETLRCEAPRMPQPT 205  
DB 115 C-VVCKNENGSPRRBHLTSVLTLIRADPPVPISITDIGHDPNV--KRIRCSASGGFPPR 171  
QY 206 VVWASQVDGANESEVSNFSFELSENVTMKVSVLVYNTINNTYSCMIENDIAKATGD 264  
DB 172 LAM---MEDGELNAV-NTYVDQDLDTLTSVSSSELDNRVNTNHSIVCLIK-----YGE 221



QY 265 IKYTE-----SEIKRSHLOLNSKASLCVSSFAISWALLPLSPYML 308  
 Db 222 LSVSQRFPWSPKQEPIDLP-----FWVITPVSGALV 256

RESULT 6

T28137  
 Ig V-region-like B-G antigen, isoform 2 - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C/Accession: T28137  
 R:Milne, S.; Kaufman, J.; Beck, S.  
 Submitted to the EMBL Data Library, May 1998  
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp  
 A:Reference number: Z20475  
 A:Accession: T28138  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-339 <MIL>  
 A:Cross-references: EMBL:AL023516; PIDN:CAA18959.1  
 C:Genetics:  
 A:Gene: B-G 2  
 A:Map position: 16  
 A:Introns: 34/1; 148/1; 183/1; 189/1; 196/1; 203/1; 210/1; 217/1; 224/1; 231/1; 239/1; 2

Query Match 9.6%; Score 151; DB 2; Length 339;  
 Best Local Similarity 21.7%; Pred. No. 0.00034;  
 Matches 56; Conservative 46; Mismatches 90; Indels 66; Gaps 10;

QY 63 SITVTYASAGNIGEDGILSCFEP--DIKLSDIVIQLKEGVIGLVEHKEGDELSEQ 120  
 Db 42 SLRYTAL-----VGODVYLCQLSPCKDAMSSD--IRWIDHRSFGVHNYONGED--LEQ 92  
 QY 121 DEMERGTAFAVDQVYGNASLRKNQLDAGTYKCYITTSKSGKANLETKGAFSMP 180  
 Db 93 MEYKRGTELRRLGSLDGNLDLRTAVSTSDSGSCAVLDGGDYADA----- 140  
 QY 181 EVNVYVNASSETLRCEAPRFPPTVW-----ASQYDQG 215  
 Db 141 --VVDELESDP-----FSQITHPKVVALAVITVILVSGFYITVFLRKKAETTKK 189  
 QY 216 ANSEVSNTEFELNS-----ENVTKVSVLYVNTVINT--YSCMIENDIAKAGDI-KVT 268  
 Db 190 GKDAELEGMDAKGTLAELEFRDPAKLETVLENERRNTEFAKTLASELERRNAQLDKLA 249  
 QY 269 ESEIKRSHLOLNSKAS 286  
 Db 250 SDLVQQTAKAVEKLNSQWS 267

RESULT 7

T28137  
 Ig V-region-like B-G antigen, isoform 1 - chicken  
 C/Species: Gallus gallus (chicken)  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C/Accession: T28137  
 R:Milne, S.; Kaufman, J.; Beck, S.  
 Submitted to the EMBL Data Library, May 1998  
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp  
 A:Reference number: Z20475  
 A:Accession: T28137  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-340 <MIL>  
 A:Cross-references: EMBL:AL023516; PIDN:CAA18958.1  
 C:Genetics:  
 A:Experimental source: clone CB12  
 A:Gene: B-G 2  
 A:Map position: 16  
 A:Introns: 34/1; 148/1; 183/1; 190/1; 197/1; 204/1; 211/1; 218/1; 225/1; 232/1; 240/1; 2

Query Match 9.6%; Score 150.5; DB 2; Length 340;  
 Best Local Similarity 32.4%; Pred. No. 0.00037;  
 Matches 35; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

QY 63 SITVTYASAGNIGEDGILSCFEP--DIKLSDIVIQLKEGVIGLVEHKEGDELSEQ 120  
 Db 42 SLRYTAL-----VGODVYLCQLSPCKDAMSSD--IRWIDHRSFGVHNYONGED--LEQ 92  
 QY 121 DEMERGTAFAVDQVYGNASLRKNQLDAGTYKCYITTSKSGKANLETKGAFSMP 168  
 Db 93 MEYKRGTELRRLGSLDGNLDLRTAVSTSDSGSCAVLDGGDYADA 140

RESULT 8

A55717  
 myelin/oligodendrocyte glycoprotein precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 08-Oct-1999  
 C/Accession: A55717; C47712  
 R:Daubas, P.; Pham-Dinh, D.; Dautigny, A.  
 Genomics 23, 36-41, 1994  
 A>Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein  
 A:Reference number: A55717; M0ID:95130110  
 A:Accession: A55717  
 A:Molecule type: DNA  
 A:Residues: 1-247 <DAU>  
 A:Cross-references: GB:L29498  
 R:Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarotti, P.; Roeckel,  
 Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993  
 A>Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglo  
 A:Reference number: A47712; M0ID:93376728  
 A:Accession: C47712  
 A:Molecule type: mRNA  
 A:Residues: 30-95, 'E', 97-247 <PHA>  
 A:Cross-references: GB:L20942; NID:g399588; PIDN:AAA03180.1; PID:g399589  
 C:Genetics:  
 A:Gene: MOG  
 A:Map position: 17  
 A>Note: encoded within the MHC  
 C:Function:  
 A:Description: may be involved in lipid interaction; may be involved in cell-cell com  
 C:Keywords: glycoprotein; myelin; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>  
 F:151-179/Domain: transmembrane #status predicted <TM>  
 F:204-229/Domain: transmembrane #status predicted <TM>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 150; DB 2; Length 247;  
 Best Local Similarity 23.8%; Pred. No. 0.00027;  
 Matches 34; Conservative 33; Mismatches 66; Indels 10; Gaps 2;

QY 37 WS-----IISIIITAGALITIGFISGRHSITVTYASAGNIGEDGILSCFEPDIK 90  
 Db 5 WSFSPSCFSLILLT-----LLOISCSYACOFRTVIGPYIRALVGEALPRLSPSGKN 60  
 QY 91 LSDIVIQLKEGVIGLVEHKEGDELSEQDEMERGTAFAVDQVYGNASLRKNQLT 150  
 Db 61 ATGGEVWYSPSRVYVHLRNCKDDQDAEPYRGTELTETISGVKYLRIQNVRS 120  
 QY 151 DAGTYKCYITTSKSGKANLETK 173  
 Db 121 DEGGYTCTFFRDHSYQEEANMEIK 143

RESULT 9

A48754  
 B7-2 antigen - human  
 N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor  
 C/Species: Homo sapiens (hmn)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 12.21 Seconds  
(without alignments)  
509,803 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574  
Sequence: 1 HASNAHGRQRQLHASTQI.....SSFAISMALLPLSPYIMLK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 2014635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/6CTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/6ackfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217.5	13.8	540	2	US-08-724-394A-4
2	212.5	13.5	610	2	US-08-724-394A-5
3	211.5	13.4	589	2	US-08-724-394A-1
4	207.5	13.2	342	2	US-08-724-394A-6
5	186	11.8	581	2	US-08-724-394A-2
6	183	11.6	581	2	US-08-724-394A-3
7	147.5	9.4	323	5	PCT-US94-09642-2
8	147.5	9.4	329	2	US-08-456-104-2
9	147.5	9.4	329	2	US-08-101-624-2
10	147.5	9.4	329	3	US-08-479-744A-2
11	147.5	9.4	329	4	US-08-280-757B-2
12	147.5	9.4	329	4	US-08-205-697A-23
13	147.5	9.4	329	4	PCT-US95-02576-23
14	144	9.1	247	5	PCT-US94-10257A-2
15	143.5	9.1	309	2	US-08-456-104-4
16	143.5	9.1	309	3	US-08-479-744A-23
17	143.5	9.1	309	4	US-08-280-757B-23
18	143.5	9.1	309	4	US-08-205-697A-21
19	143.5	9.1	309	5	PCT-US95-02576-21
20	143.5	9.1	314	4	US-08-205-697A-13
21	143.5	9.1	314	5	PCT-US95-02576-13
22	132	8.4	478	5	PCT-US95-08493-13
23	132	8.4	860	5	PCT-US95-08493-19
24	132	8.4	868	1	US-08-374-834-1
25	132	8.4	868	2	US-08-644-271-1
26	132	8.4	868	5	PCT-US95-08493-21
27	128	8.1	365	4	US-08-928-383B-23

28	128	8.1	365	4	US-08-928-383B-24	Sequence 24, Appl
29	127	8.1	946	5	PCT-US95-08493-13	Sequence 13, Appl
30	124.5	7.9	208	3	US-08-630-172-15	Sequence 15, Appl
31	124	7.9	306	2	US-08-147-772-4	Sequence 4, Appl
32	124	7.9	306	2	US-08-456-104-8	Sequence 8, Appl
33	124	7.9	306	2	US-08-101-624-25	Sequence 2, Appl
34	124	7.9	306	3	US-08-153-262-4	Sequence 4, Appl
35	124	7.9	306	3	US-08-479-744A-31	Sequence 31, Appl
36	124	7.9	306	4	US-08-280-757B-31	Sequence 31, Appl
37	124	7.9	306	4	US-09-159-135-4	Sequence 4, Appl
38	124	7.9	306	4	US-08-205-697A-17	Sequence 17, Appl
39	124	7.9	306	5	PCT-US95-02576-17	Sequence 17, Appl
40	124	7.9	320	5	US-08-205-697A-2	Sequence 2, Appl
41	124	7.9	320	5	PCT-US95-02576-2	Sequence 2, Appl
42	123.5	7.8	869	1	US-08-374-834-16	Sequence 16, Appl
43	123.5	7.8	869	2	US-08-644-271-29	Sequence 29, Appl
44	123	7.8	365	4	US-08-928-383B-26	Sequence 26, Appl
45	123	7.8	467	2	US-07-916-098A-45	Sequence 45, Appl

## ALIGNMENTS

RESULT 1  
US-08-724-394A-4  
; Sequence 4, Application US/08724394A  
; Patent No. 5872237  
; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
; APPLICANT: Kronmal, Gregory S.  
; APPLICANT: Lauer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
; TITLE OF INVENTION: Sequences and Antibodies Thereo  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 017957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..540  
; OTHER INFORMATION: /note="BTF5"  
; US-08-724-394A-4

Query Match 13.8%; Score 217.5; DB 2; Length 540;  
Best Local Similarity 25.6%; Pred. No. 6.6e-14;  
Matches 56; Conservative 45; Mismatches 101; Indels 17; Gaps 7;  
QY 62 HSITVTYASAGNT----GEGDILSCTFEPDIKLSDIYQMLKEGYGLVHEFKGKDEL 117  
DB 30 HSAQSVSLGPPSPILAMVGEDADLPCHLEPTMSAETMELRWSSSLRQVYVYADGKEVE 89  
QY 118 SPQDMFGRGTAVFADQYVGNASRLKRVQLTDAGTKCYIITSKGNANLEYKTGAF 177  
DB 90 DRQSPKRSITLIDGLTAGKALRIHNVYASDSGKYLCTFQDDGYEKALVELKVAL 149  
QY 178 SNEPVND---YNASSETLKEAPRFPQPTVYVMAQVDOGANFSEVNTSELSNENT 234  
DB 150 G-SDLHVQKVGKDGDIHLECRSTGMYPPQIQWNSN--NKGNN---IPVYEA PVVADGVC 203  
QY 235 MKVY--SVLYNTTINNTSCMIENDI--AKATGDIKYTE 269  
DB 204 LYAVASVIMRSGSGVSCIRSSILGLEKTAISISIAD 242

## RESULT 2

US-08-724-394A-5

Sequence 5, Application US/08724394A  
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Krommal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724.394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 610 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..610

OTHER INFORMATION: /note= "BTF3"

Query Match 13.5%; Score 212.5; DB 2; Length 610;  
Best Local Similarity 25.7%; Pred. No. 2.6e-13;  
Matches 52; Conservative 42; Mismatches 95; Indels 13; Gaps 6;  
QY 75 IEDGILSCTFEPDIKLSDIYQMLKEGYGLVHEFKGKDELSDQDMFGRGTAVFADQ 134  
DB 47 VGEDADLPCHLEPTMSAETMELRWSSSLRQVYVYADGKEVEDRQSAFVRSRTSILRDG 106  
QY 135 VVGNASRLKRVQLTDAGTKCYIITSKGNANLEYKTGAFSNEPVND---YNASSE 191  
DB 107 TAGKALRIHNVYASDSGKYLCTFQDDGYEKALVELKVALG-SDLHEVKGTEDEGI 165  
QY 192 TLRCAPRFPQPTVYVMAQVDOGANFSEVNTSELSNENTMKVY--SVLYNTTINNT 249  
DB 166 HLECRSTGMYPPQIQWNSN--TKGENIPAV---EAPVYADGCVGLAVASVIMRSGSGC 220  
QY 250 VSCMIENDI--AKATGDIKYTE 269  
DB 221 VSCIIRSSILGLEKTAISISIAD 242

## RESULT 3

US-08-724-394A-1

Sequence 1, Application US/08724394A  
Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Krommal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724.394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..589

OTHER INFORMATION: /note= "BT"

US-08-724-394A-1

Query Match 13.48; Score 211.5; DB 2; Length 589;  
Best Local Similarity 26.68; Pred. No. 3.1e-13;  
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

OY 75 IGEDILSCFEPEPKIKSDIYIOMLKEGVGLIYHEFEKGEKDELSPDDEMRGRTAVFADQ 134  
DB 45 VGEDEALFCRISPNASAHLEIRMFRRKVSAPVLYHRGRQDEADQMPERYGRATLYVDG 104  
OY 135 VIVGNASLRKLVOLTDAGYKCYIITSKGGKNNLEKYGAF-SMPEVNV-DYNASSET-T 192  
DB 105 IAKGVVALRINGVRSDDGEYTCFREDGSEELVHLKVALGSDPHISMQVQENGECIC 164  
OY 193 LRCEAPRPFPPQTYVWASQVDOGANFSEVSNTSELSNENVTMKVSVLYNVFTINNTYSC 252  
DB 165 LECTSVGVYPPPOVOW-RTSKGEKFPSTSE-SRNPDEGLFTVAASVILINDTSTKNVSC 221  
OY 253 MIEN 256  
DB 222 YION 225

RESULT 4  
US-08-724-394A-6  
Sequence 6, Application US/08724394A  
Patent No. 5872237  
GENERAL INFORMATION:  
APPLICANT: Feder, John N.  
APPLICANT: Krommal, Gregory S.  
APPLICANT: Lauer, Peter M.  
APPLICANT: Ruddy, David A.  
APPLICANT: Thomas, Winston  
APPLICANT: Tsuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
TITLE OF INVENTION: Sequences and Antibodies Thereo  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,394A  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Flits, Renee A.  
REGISTRATION NUMBER: 35,136  
REFERENCE/DOCKET NUMBER: 017957-000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..342  
OTHER INFORMATION: /note= "BFP4"  
US-08-724-394A-6

Query Match 13.28; Score 207.5; DB 2; Length 342;  
Best Local Similarity 26.18; Pred. No. 3.4e-13;  
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

OY 75 IGEGLILSCFEPEPKIKSDIYIOMLKEGVGLIYHEFEKGEKDELSPDDEMRGRTAVFADQ 134  
DB 47 VGEDEADLPCHLPYMASETMELKWSSSLROVNVNADGKEVEDROSAPYRGRTSILRDG 106  
OY 135 VIVGNASLRKLVOLTDAGYKCYIITSKGGKNNLEKYGAF-SMPEVNV-DYNASSET 192  
DB 107 ITAKKALRIHNTVADSOGKTCYCFQDGDYERKALVELKVALGSDPHISMQVQENGECIC 166  
OY 193 LRCEAPRPFPPQTYVWASQVDOGANFSEVSNTSELSNENVTMKVSVLYNVFTINNTYSC 240  
DB 167 LECTSVGVYPPPOVOW-RTSKGEKFPSTSE-SRNPDEGLFTVAASVILINDTSTKNVSC 221  
OY 241 LYNTINNTYSCMIENDI-AKATGDIKYE 269  
DB 212 IMRGSGEVSCLIRNSLIGLEKTASISID 242

RESULT 5  
US-08-724-394A-2  
Sequence 2, Application US/08724394A  
Patent No. 5872237  
GENERAL INFORMATION:  
APPLICANT: Feder, John N.  
APPLICANT: Krommal, Gregory S.  
APPLICANT: Lauer, Peter M.  
APPLICANT: Ruddy, David A.  
APPLICANT: Thomas, Winston  
APPLICANT: Tsuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
TITLE OF INVENTION: Sequences and Antibodies Thereo  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,394A  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Flits, Renee A.  
REGISTRATION NUMBER: 35,136  
REFERENCE/DOCKET NUMBER: 017957-000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..581  
OTHER INFORMATION: /note= "BFP1"  
US-08-724-394A-2

Query Match 11.8%; Score 186; DB 2; Length 581;  
Best Local Similarity 23.6%; Pred. No. 1.3e-10;  
Matches 52; Conservative 41; Mismatches 115; Indels 12; Gaps 5;

QY 42 IITLGAALIIIGFISGHSITVTVASAGNIGEDGIISCTEPEDIKISDIYIOWLKE 101  
DB 19 LLLLLLSLCLAL-----VSAOFIVVGPDPDLATVAGENTTLRCHLSPEKNAEDMEVWFRS 73  
QY 102 GVLGLVHEFEKDELSEODEMGRFAVADQVIVGNLSRLKNQVOLDAGTYKCYIIT 161  
DB 74 QBPAPVYIKGKERTEOMEETRGRTTYSKDISRSVALVHNITAOENGTYRCYFDE 133  
QY 162 SKKGANALE-YKTGAFSMEPVNV-DYNASSETLRCEAPRFPQPTVVMASQVDOGA-NF 218  
DB 134 GRVYDEILHLVAVAGLSKRLISMRGHEDGIRLECLISRWYKPKPLVWRDPYGVAPAL 193  
QY 219 SEVSNTSFEIENSENTKRVSVLYVNTINTYSCMIENDI 258  
DB 194 KEYSMP-----DADGLFMVTTAVIIRDKSVRNMSCSINTL 229

RESULT 6  
US-08-724-394A-3  
Sequence 3, Application US/08724394A  
Patent No. 5872237  
GENERAL INFORMATION:  
APPLICANT: Feder, John N.  
APPLICANT: Krommal, Gregory S.  
APPLICANT: Laufer, Peter M.  
APPLICANT: Ruddy, David A.  
APPLICANT: Thomas, Winston  
APPLICANT: Tsuchihashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el  
TITLE OF INVENTION: Sequences and Antibodies Thereeto  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,394A  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitts, Renee A.  
REGISTRATION NUMBER: 35,136  
REFERENCE/DOCKET NUMBER: 017957-000100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1.581  
OTHER INFORMATION: /note= "BTF2"  
US-08-724-394A-3

Query Match 11.6%; Score 183; DB 2; Length 581;  
Best Local Similarity 23.6%; Pred. No. 2.6e-10;  
Matches 59; Conservative 42; Mismatches 113; Indels 36; Gaps 8;

QY 23 EPSPAN-----ASLGQILFWSIIISIIIIAGAILIIGFISGRHSITVTVASAGNT-- 75  
DB 2 EPAAALHFEPLASL-----LLLLLLLSLICALV-----SAGPTVGPANPLIA 45  
QY 76 --GEODILSCTEPEDIKISDIYIOWLKEGVLLVHFEKRGKDELSEODEMGRFAVAD 133  
DB 46 WGEENTLRLCHLSPEKNAEDMEVWFRSQSPAPVYKGGRETERTEOMEETRGRTTYSK 105  
QY 134 QVIVGNASRLKNQVOLDAGTYKCYIITSKGKANALE-YKTGAFSMEPVND-YNASSE 191  
DB 106 DINRGVALVHNITVQENGITRCYFQEGRSYDEALRLVAVAGLSKPLIEIKAOEDSI 165  
QY 192 TLRCAPRMPFPQPTVVMASQVDOGANFSEVSNTSFEI--NSENTMKRVSVLYVNTINN 248  
DB 166 WLECISGVYPEPLVWRDP-----YGEVVPALKEVSIADADGLFMVTTAVIIRDKYVR 219  
QY 249 TYSCTMIENDI 258  
DB 220 NVSCSVNNTL 229

RESULT 7  
PCT-US94-09642-2  
Sequence 2, Application PC/TUS9409642  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding  
TITLE OF INVENTION: Protein and Related Reagents  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation, M-3-W  
STREET: One Giralda Farms  
CITY: Madison  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07940-1000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh IIcx  
OPERATING SYSTEM: System Software 7.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09642  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/120,606  
FILING DATE: 13-SEP-1993  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US 08/116,882  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Blasdale, John H. C.  
REGISTRATION NUMBER: 31,895  
REFERENCE/DOCKET NUMBER: DX0390K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-822-7398  
TELEFAX: 201-822-7039  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 323 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-09642-2













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APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.

EQ ID NO 415  
LENGTH: 65

> 0 <  
01 10 IntelliGenetics  
> 0 <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file US09617747.res made by sedavid on Mon 23 Jul 101 13:49:45-PDT.

Query sequence being compared:US-09-636-801-392 (1-309)  
Number of sequences searched: 68  
Number of scores above cutoff: 68

Results of the initial comparison of US-09-636-801-392 (1-309) with:  
File : US09617747.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
O -  
U -  
E -  
N -  
C -  
E -  
S 0-  
SCORE 0 34 69 103 137 172 206 240 275 309  
STDY 1 2 3 4 5 6 7 8

## PARAMETERS

Similarity matrix PAM-150 K-tuple 2  
Threshold level of sim. 16%  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 0  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 18 Median 11 Standard Deviation 37.06  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 4444  
Number of sequences searched: 68  
Number of scores above cutoff: 68

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Opt.	Length	Score	Score	Sig.	Frame
---------------	-------------	------------	--------	-------	-------	------	-------

1. US-09-617-747-39 Sequence 392, Application 309 309 309 7.85 0  
The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Sig.	Frame
2. US-09-617-747-39 Sequence 393, Application 282 282 282 7.12 0	**** 7 standard deviations above mean **** **** 1 standard deviation above mean **** **** 0 standard deviation from mean ****	65	65	65	1.27	0
3. US-09-617-747-41 Sequence 415, Application 65 65 65 1.27 0		65	65	65	1.27	0
4. US-09-617-747-41 Sequence 413, Application 35 36 36 0.49 0		35	36	36	0.49	0
5. US-09-617-747-41 Sequence 402, Application 35 35 35 0.46 0		35	35	35	0.46	0
6. US-09-617-747-40 Sequence 402, Application 21 22 22 0.11 0		21	22	22	0.11	0
7. US-09-617-747-41 Sequence 412, Application 20 21 21 0.08 0		20	21	21	0.08	0
8. US-09-617-747-41 Sequence 411, Application 20 21 21 0.08 0		20	21	21	0.08	0
9. US-09-617-747-40 Sequence 405, Application 20 21 21 0.08 0		20	21	21	0.08	0
10. US-09-617-747-39 Sequence 399, Application 20 21 21 0.08 0		20	21	21	0.08	0
11. US-09-617-747-39 Sequence 398, Application 20 21 21 0.08 0		20	21	21	0.08	0
12. US-09-617-747-41 Sequence 410, Application 20 20 20 0.05 0		20	20	20	0.05	0
13. US-09-617-747-40 Sequence 403, Application 20 20 20 0.05 0		20	20	20	0.05	0
14. US-09-617-747-40 Sequence 401, Application 20 20 20 0.05 0		20	20	20	0.05	0
15. US-09-617-747-40 Sequence 400, Application 20 20 20 0.05 0		20	20	20	0.05	0
16. US-09-617-747-39 Sequence 397, Application 20 20 20 0.05 0		20	20	20	0.05	0
17. US-09-617-747-39 Sequence 395, Application 20 20 20 0.05 0		20	20	20	0.05	0
18. US-09-617-747-39 Sequence 394, Application 20 20 20 0.05 0		20	20	20	0.05	0
19. US-09-617-747-40 Sequence 409, Application 20 19 19 0.03 0		20	19	19	0.03	0
20. US-09-617-747-40 Sequence 408, Application 20 19 19 0.03 0		20	19	19	0.03	0
21. US-09-617-747-40 Sequence 407, Application 20 19 19 0.03 0		20	19	19	0.03	0
22. US-09-617-747-40 Sequence 406, Application 20 19 19 0.03 0		20	19	19	0.03	0
23. US-09-617-747-40 Sequence 404, Application 20 19 19 0.03 0		20	19	19	0.03	0
24. US-09-617-747-39 Sequence 396, Application 20 19 19 0.03 0		20	19	19	0.03	0
25. US-09-617-747-43 Sequence 431, Application 10 11 11 0.19 0		10	11	11	0.19	0
26. US-09-617-747-42 Sequence 428, Application 10 11 11 0.19 0		10	11	11	0.19	0
27. US-09-617-747-42 Sequence 425, Application 10 11 11 0.19 0		10	11	11	0.19	0
28. US-09-617-747-42 Sequence 422, Application 10 11 11 0.19 0		10	11	11	0.19	0
29. US-09-617-747-45 Sequence 450, Application 9 10 10 0.22 0		9	10	10	0.22	0
30. US-09-617-747-44 Sequence 449, Application 9 10 10 0.22 0		9	10	10	0.22	0
31. US-09-617-747-44 Sequence 447, Application 9 10 10 0.22 0		9	10	10	0.22	0
32. US-09-617-747-44 Sequence 442, Application 9 10 10 0.22 0		9	10	10	0.22	0
33. US-09-617-747-43 Sequence 436, Application 9 10 10 0.22 0		9	10	10	0.22	0
34. US-09-617-747-43 Sequence 435, Application 10 10 10 0.22 0		10	10	10	0.22	0
35. US-09-617-747-43 Sequence 434, Application 10 10 10 0.22 0		10	10	10	0.22	0
36. US-09-617-747-43 Sequence 433, Application 10 10 10 0.22 0		10	10	10	0.22	0
37. US-09-617-747-43 Sequence 432, Application 10 10 10 0.22 0		10	10	10	0.22	0
38. US-09-617-747-43 Sequence 430, Application 10 10 10 0.22 0		10	10	10	0.22	0
39. US-09-617-747-42 Sequence 429, Application 10 10 10 0.22 0		10	10	10	0.22	0
40. US-09-617-747-42 Sequence 427, Application 10 10 10 0.22 0		10	10	10	0.22	0
41. US-09-617-747-42 Sequence 426, Application 10 10 10 0.22 0		10	10	10	0.22	0
42. US-09-617-747-42 Sequence 424, Application 10 10 10 0.22 0		10	10	10	0.22	0
43. US-09-617-747-42 Sequence 423, Application 10 10 10 0.22 0		10	10	10	0.22	0
44. US-09-617-747-42 Sequence 421, Application 10 10 10 0.22 0		10	10	10	0.22	0
45. US-09-617-747-41 Sequence 418, Application 10 10 10 0.22 0		10	10	10	0.22	0
46. US-09-617-747-41 Sequence 419, Application 10 10 10 0.22 0		10	10	10	0.22	0
47. US-09-617-747-41 Sequence 417, Application 10 10 10 0.22 0		10	10	10	0.22	0
48. US-09-617-747-41 Sequence 416, Application 10 10 10 0.22 0		10	10	10	0.22	0
49. US-09-617-747-39 Sequence 390, Application 10 51 51 0.22 0		10	51	51	0.22	0
50. US-09-617-747-38 Sequence 389, Application 10 51 51 0.22 0		10	51	51	0.22	0
51. US-09-617-747-31 Sequence 312, Application 914 10 51 0.22 0		914	10	51	0.22	0
52. US-09-617-747-45 Sequence 455, Application 9 9 9 0.24 0		9	9	9	0.24	0
53. US-09-617-747-45 Sequence 454, Application 9 9 9 0.24 0		9	9	9	0.24	0
54. US-09-617-747-45 Sequence 453, Application 9 9 9 0.24 0		9	9	9	0.24	0
55. US-09-617-747-45 Sequence 451, Application 9 9 9 0.24 0		9	9	9	0.24	0
56. US-09-617-747-45 Sequence 452, Application 9 9 9 0.24 0		9	9	9	0.24	0
57. US-09-617-747-44 Sequence 448, Application 9 9 9 0.24 0		9	9	9	0.24	0
58. US-09-617-747-44 Sequence 446, Application 9 9 9 0.24 0		9	9	9	0.24	0
59. US-09-617-747-44 Sequence 445, Application 9 9 9 0.24 0		9	9	9	0.24	0
60. US-09-617-747-44 Sequence 444, Application 9 9 9 0.24 0		9	9	9	0.24	0
61. US-09-617-747-44 Sequence 443, Application 9 9 9 0.24 0		9	9	9	0.24	0
62. US-09-617-747-44 Sequence 441, Application 9 9 9 0.24 0		9	9	9	0.24	0
63. US-09-617-747-44 Sequence 440, Application 9 9 9 0.24 0		9	9	9	0.24	0



Sequence 412, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 412

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300 X  
VLYNVTINNTSCMIENDIAKATGDIKVTSEIKRSHQLLNSKASLCVSEFAISWALLPLSPYLMK  
|||||  
SSFAISWALLPLSPYLMK  
X  
10 20

8. US-09-636-801-392 (1-309)

US-09-617-747-41 Sequence 411, Application US/09617747

Sequence 411, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 411

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300 X  
VTMKVSVLYNVTINNTSCMIENDIAKATGDIKVTSEIKRSHQLLNSKASLCVSEFAISWALLPLSP  
|||||  
SKASLCVSEFAISWALLPL  
X  
10 20

YLMK

9. US-09-636-801-392 (1-309)

US-09-617-747-40 Sequence 405, Application US/09617747

Sequence 405, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 405

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

150 160 170 180 190 200 210 X  
RLKNQULDAGTYKCYIIITISKGNANLETKGATSMPEVNDYNASSETLRCGAPRRFPPTVYMASOYD  
|||||  
LRCGAPRRFPPTVYMASOY  
X  
10 20

220 230 240 250 260  
GANFSEVNSTSELSNENVTMKYVSVLYNVTINNTSCMIENDIAKAT

10. US-09-636-801-392 (1-309)

US-09-617-747-39 Sequence 399, Application US/09617747

Sequence 399, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 399

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

60 70 80 90 100 110 120 X  
IIGFISGRHSITVTVASAGNIGEDGILCTFEPDILSDIVIQWLKEGVGLVHERKEGKDELSEDEMF  
|||||  
VLGLVHERKEGKDELSEDEMF  
X  
10 20

130 140 150 160 170  
RGTRAVFADQVIYVGNASLRLKNVQLTDAGTYKCYIITISKGNANLEY

TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 65 Optimized Score - 65 Significance - 1.27  
Residue Identity - 100% Matches - 65 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

120 130 140 150 160 170 180  
GKDELSEODEMFRGRTAVFADQIVYGNASLRKLVOLTDAQYKCYITTSKGGNANLEKYGAFSPMEVNV  
|||||  
KGGNANLEKYGAFSPMEVNV  
X  
10 20

190 200 210 220 230 240 250  
DYASSETLRCEAPRMFPPOPTVYMASOVDOGANFSEVNTSMKVVSYLVNTINNYSCHMEN  
|||||  
DYASSETLRCEAPRMFPPOPTVYMASOVDOGANFSEVNTSFE  
30 40 50 60 X

260 270  
DIAKATGDIKVTESEIKRRSH

4. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 414, Application US/09617747

Sequence 414, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 414  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 36 Optimized Score - 36 Significance - 0.49  
Residue Identity - 100% Matches - 35 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

60 70 80 90 100 X 110 120  
IIGFGISGRHSITVTYASAGNIGEDGILSCFEPDIKLSIDIYIOMLKEGVGLVHFEKGGKDELSEODEMF  
|||||  
VLGLVHFEKGGKDELSEODEMF  
X  
10 20

130 140 150 160 170 180  
RGRTAVFADQIVYGNASLRKLVOLTDAQYKCYITTSKGGNANLEKYGAFSPMEVNVNDYN  
|||||  
RGRTAVFADQIVY  
30 X

5. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 413, Application US/09617747

Sequence 413, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 413  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 35 Optimized Score - 35 Significance - 0.46  
Residue Identity - 100% Matches - 35 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

10 20 30 40 50 60 70  
GRORQLHSASTOIRWERSPAMASIGOTLFWISITITITLAGATALLIGFGISGRHSITVTYASAGNIGEDG  
|||||  
ISGRHSITVTYASAGNIGEDG  
X  
10 20

80 90 X 100 110 120 130 140  
ILSCFEPDIKLSIDIYIOMLKEGVGLVHFEKGGKDELSEODEMFRGRTAVFADQIVYGNASL  
|||||  
ILSCFEPDIKLS  
30 X

6. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 402, Application US/09617747

Sequence 402, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 402  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 22 Optimized Score - 22 Significance - 0.11  
Residue Identity - 100% Matches - 21 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

100 110 120 130 140 150 160 X  
OMLKEGVGLVHFEKGGKDELSEODEMFRGRTAVFADQIVYGNASLRKLVOLTDAQYKCYITTSKGGN  
|||||  
VOLTDAQYKCYITTSKGGN  
X  
10 20

170 180 190 200 210  
NLEKYGAFSPMEVNVNDYNASSETLRCEAPRMFPPOPTVYMASOVDOGAN

7. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 412, Application US/09617747

160 170 180 190 200  
X 10 20  
YKCYITTSKGNANLEFKTGAFSMPEVAVDYNASSFTLRCAFRMP

15. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 400, Application US/09617747

Sequence 400, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 400  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

70 80 90 100 110 120 130 X  
TVASAGNIGEDGILSCFEPDIKLSDIVIOMKEGVLGVHEFKGKDELSDQEMFRGRTAVFADQVIVGN  
|||||  
SDQEMFRGRTAVFADQVIV  
X 10 20

140 150 160 170 180  
ASLRLLKNVQLTDAGTYKCYITTSKGNANLEFKTGAFSMPEVAVDYN

16. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 397, Application US/09617747

Sequence 397, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 397  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 X 80 90 X

EPSPAMASIGQILFWISIISIIILLAGAIALIIGFISGRHSITVTTVASAGNIGEDGILSCFEPDIKLSDI  
|||||  
GNIGEDGILSCFEPDIKLS  
X 10 20

17. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 395, Application US/09617747

Sequence 395, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 395  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 60 X 70  
HSAASAGRQRLHSASTQIRWEPSPAMASIGQILFWISIISIIILLAGAIALIIGFISGRHSITVTTVASA  
|||||  
IIILAGAILIIGFISGRH  
X 10 20

80 90 100 110  
GNIGEDGILSCFEPDIKLSDIVIOMKEGVLGVHEFK

18. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 394, Application US/09617747

Sequence 394, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 394  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05  
Residue Identity = 100% Matches = 20 Mismatches = 0

11. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 398, Application US/09617747

Sequence 398, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 398  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 21 Optimized Score - 21 Significance - 0.08  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

40 50 60 70 80 90 100 X  
SISIIILGAILIIGISGRHSITVTVASAGNIGEDGILSCFEPDIKISDIYIOWLKEGVLGVIHE  
|||||  
DIXLSDIYIOWLKEGVLGVI  
X 10 20

110 120 130 140 150  
EKEGDELSEODEMFRGRTAVFAFADQVIYGNASLRKKNVQLTDAGTYKC

12. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 410, Application US/09617747

Sequence 410, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 410  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 20 Optimized Score - 20 Significance - 0.05  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

220 230 240 250 260 270 280 X  
FSEVSNFSFELNSNVMKYVSVLYNTINTYSCMIENDAKAKATGDIKVESIKRRSHQLLNKRSALCV  
|||||  
TESEIKRRSHQLLNKRSAL  
X 10 20

290 300

SSFFAISWALLPLSPYMLK

13. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 403, Application US/09617747

Sequence 403, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 403  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 20 Optimized Score - 20 Significance - 0.05  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

120 130 140 150 160 170 180 X  
GKDELSEODEMFRGRTAVFAFADQVIYGNASLRKKNVQLTDAGTYKCIITTSKGNANLEYKTGAFSMEVAV  
|||||  
KGGANLEYKTGAFSMEV  
X 10 20

190 200 210 220 230  
DYNASSETLRCEARPMFPQPTVWASQVDOGANSFSEVSNFSFELNSN

14. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 401, Application US/09617747

Sequence 401, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 401  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 20 Optimized Score - 20 Significance - 0.05  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

90 100 110 120 130 140 150 X  
CTFEPDIKISDIYIOWLKEGVLGVHEKCKDELSEODEMFRGRTAVFAFADQVIYGNASLRKKNVQLTDAGT  
|||||  
DOYIVGNASLRKKNVQLTDA

LENGTH: 20  
TYPE: PR1  
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

160 170 180 190 200 210 220 X  
YIITSKGNANLEKTKGAFSMPEVNDVYNASSSETLRCEAPRFQPIVWASQVDOGANFSEVNTSELN  
|||||  
WASQVDOGANFSEVNTSEFE  
X  
10

230 240 250 260 270  
SENVTMKVYSVLYNTINTNTYSCTMIENDIAKATGDIKYTESEIKRRSH

23. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 404, Application US/09617747

Sequence 404, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 404

LENGTH: 20  
TYPE: PR1  
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 190 X  
TAVFADQYIVGNASLRKKNVOLTDACTYKCYIITSKGNANLEKTKGAFSMPEVNDVYNASSSETLRCEAPR  
|||||  
SMPEVNDVYNASSSETLRCEA  
X  
10

200 210 220 230 240  
WFPQTVWASQVDOGANFSEVNTSEFLNSENVTMKVYSVLYNTIN

24. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 396, Application US/09617747

Sequence 396, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 396  
LENGTH: 20  
TYPE: PR1  
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03  
Residue Identity = 100% Matches = 20 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70 X  
GROFOLHSASTQIRWEPSPAMASLGQLFWISITSIITLACALILIGFGISGRSITVTYVNASGNIGEDG  
|||||  
ISGRSITVTYVNASGNIG  
X  
10

80 90 100 110 120  
ILSCFEPDIKLSDIVIQWLKKGVLGVHFEFEGKDELSEODEMRGR

25. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 431, Application US/09617747

Sequence 431, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 431

LENGTH: 10  
TYPE: PR1  
ORGANISM: Homo sapiens

Initial Score = 11 Optimized Score = 11 Significance = -0.19  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X  
GAILILIGFGISGRSITVTYVNASGNIGEDGILSCFEPDIKLSDIVIQWLKKGVLGVHFEFEGKDELSE  
|||||  
WLKKGVLGV  
X  
10

120 130 140 150  
ODEMRGRRTAVFADQYIVGNASLRKKNVOLTDACTYK

26. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 428, Application US/09617747

Sequence 428, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17

Gaps - 0 Conservative Substitutions - 0

10 20 30 40 50 60 70  
HASAHSGRQRLHSASTQIRWEPSPAMSLGQILFWSTIIIIIIILGALALLIGRISGRHSITVTVASA  
|||||  
MASLQILFWSTIIIIIIILA  
X 10 20

80 90  
GNIGEDGILSCTEFPDRIKSDIYIO

19. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 409, Application US/09617747

Sequence 409, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 409  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

210 220 230 240 250 X 260 270 X  
QPTVWASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNVTINNYSMIENDAKATGDIKVTSEIKR  
|||||  
MIENDAKATGDIKVTSEI  
X 10 20

280 290 300  
RSHQLLNKSKASLCVSSFALISWALLPLSPYMLK

20. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 408, Application US/09617747

Sequence 408, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 408  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

190 200 210 220 230 240 250 X  
ASSETLRCEAPRWFPPQPTVWASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNVTINNYSMIENDIA  
|||||  
VSVLYNVTINNYSMIEND  
X 10 20

260 270 280 290 300  
KATGDIKVTSEIKRSHQLLNKSKASLCVSSFALISWALLPLSPYML

21. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 407, Application US/09617747

Sequence 407, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 407  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03  
Residue Identity - 100% Matches - 20 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

180 190 200 210 220 X 230 240 X  
KTGAFSMPEVNVDMASSELRLRCAPRWFPPQPTVWASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNV  
|||||  
NTSEFELNSENVTMKVSVLY  
X 10 20

250 260 270 280 290  
TINNYSMIENDAKATGDIKVTSEIKRSHQLLNKSKASLCVSSF

22. US-09-636-801-392 (1-309)  
US-09-617-747-40 Sequence 406, Application US/09617747

Sequence 406, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 406

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X 110  
ILAAIALLIGISGRHSITVTYASAGNIGEDGIIISCTFEPDIKLSDIYIOMLKGVGLVHEFEKGEDELSE  
|||||  
VIOMLKGV  
X

120 130 140 150  
LSEDEMERGRHTAVFADQVYGNASLRKKNVQLTDAG

31. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 447, Application US/09617747

Sequence 447, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 435

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 447

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

250 260 270 280 290 300 X  
TYSCEMIENDIAKATGDIKVTSEIKRSHLQLNSKASLCVSSFFAISWALLPLSPYLMLK  
|||||  
LLPLSPYL  
X  
X

32. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 442, Application US/09617747

Sequence 442, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 442

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X 110  
GAIALLIGISGRHSITVTYASAGNIGEDGIIISCTFEPDIKLSDIYIOMLKGVGLVHEFEKGEDELSE  
|||||  
WLKGVGL  
X

120 130 140 150  
ODEMERGRHTAVFADQVYGNASLRKKNVQLTDAGTYK

33. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 436, Application US/09617747

Sequence 436, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 435

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 436

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

250 260 270 280 290 300 X  
NTYSCMIENDIAKATGDIKVTSEIKRSHLQLNSKASLCVSSFFAISWALLPLSPYLMLK  
|||||  
ALLPLSPYL  
X  
X

34. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 435, Application US/09617747

Sequence 435, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 435

FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617.747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 428

LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	=	11	Optimized Score	=	11	Significance	=	-0.19
Residue Identity	=	100%	Matches	=	10	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			0

250 260 270 280 290 300 X  
NTYSCMIENDIAKATGDIKVTSEIKRSHQLNLSKASLCVSSFFAISMALLPLSPYLMK  
|||||  
ALLPLSPYLM  
X 10

## 27. US-09-636-801-392 (1-309)

US-09-617-747-42 Sequence 425, Application US/09617747

Sequence 425, Application US/09617747

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617.747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 425  
LENGTH: 10  
TYPE: PRT

ORGANISM: Homo sapiens

Initial Score	=	11	Optimized Score	=	11	Significance	=	-0.19
Residue Identity	=	100%	Matches	=	10	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			0

250 260 270 280 290 300 X  
NNTYSCMIENDIAKATGDIKVTSEIKRSHQLNLSKASLCVSSFFAISMALLPLSPYLMK  
|||||  
WALLPLSPYL  
X 10

## 28. US-09-636-801-392 (1-309)

US-09-617-747-42 Sequence 422, Application US/09617747

Sequence 422, Application US/09617747

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617.747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 422

LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	=	11	Optimized Score	=	11	Significance	=	-0.19
Residue Identity	=	100%	Matches	=	10	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			0

250 260 270 280 290 300 X  
TYSCMIENDIAKATGDIKVTSEIKRSHQLNLSKASLCVSSFFAISMALLPLSPYLMK  
|||||  
LLPLSPYLM  
X 10

## 29. US-09-636-801-392 (1-309)

US-09-617-747-45 Sequence 450, Application US/09617747

Sequence 450, Application US/09617747

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617.747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 450  
LENGTH: 9  
TYPE: PRT

ORGANISM: Homo sapiens

Initial Score	=	10	Optimized Score	=	10	Significance	=	-0.22
Residue Identity	=	100%	Matches	=	9	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			0

250 260 270 280 290 300 X  
VTNNYSCMIENDIAKATGDIKVTSEIKRSHQLNLSKASLCVSSFFAISMALLPLSPYLMK  
|||||  
ATSMALLPL  
X

## 30. US-09-636-801-392 (1-309)

US-09-617-747-44 Sequence 449, Application US/09617747

Sequence 449, Application US/09617747

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617.747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 449



FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 430

LENGTH: 10  
TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 80 90 100  
SLGGLFWSIIIIIIAGALALIGICGRHSITVTYVASAGNIGEDICSTCEPDKLSDIYIOWLKE  
|||||  
IIISCTEEPDI  
X  
10

110 120 130  
GVLDLVHFEKGEKDELSEODEMFRGRTAVFADQYIVGN

39. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 429, Application US/09617747

Sequence 429, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 429

LENGTH: 10

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

230 240 250 260 270 280 290 300  
NSENVTKVSVLYNTINNTYSCMIENDIAKATGDIKYESEIKRSHLOLNKSKASLCSVSFFAISMALL  
|||||  
OLNLSKASLSC  
X  
10

PLSPYLMK

40. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 427, Application US/09617747

Sequence 427, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 427

LENGTH: 10

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22

Residue Identity = 100% Matches = 10 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

100 110 120 130 140 150 X  
WLKEGVLDLVHFEKGEKDELSEODEMFRGRTAVFADQYIVGNASRLKNVOLTDAQYKCYITISKGNAN  
|||||  
QUTDAGTYKC  
X  
10

170 180 190 200  
LEYKTGAFSMPEVNDYNASSSETLRCEAPRWPQPTV

41. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 426, Application US/09617747

Sequence 426, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 426

LENGTH: 10

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
HASAHASGRQRLHSASTQIRWPPSPAMSLGQILFWSIIIIIIIIAGALALIGICGRHSITVTYVASA  
|||||  
IIIIIIIIII  
X  
10

80 90 100  
GNIGEGIIISCTFEPIKLSDIYIOWLKEGV

42. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 424, Application US/09617747

Sequence 424, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

LENGTH: 10  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

40 50 60 70 80 90 100  
LEWSTIIIIIIAGAILIIGFGISGRHSITVTYVASAGNIGEDGILSCFEPDIKLSDIYQWLKEGVGL  
|||||||  
FEPDIKLSDI  
X  
10

110 120 130 140  
VHEFEKGDELSEQDEMERGRKTAIVADQYIVGNASLRL

35. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 434, Application US/09617747

Sequence 434, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 434  
LENGTH: 10  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
SGHROHLSASTOIRNEPSPAMASLGQILFWSIIIIIIIIAGAILIIGFGISGRHSITVTYVASAGNIGED  
|||||||  
GISGRHSITV  
X  
10

80 90 100 110  
GILSCFEPDIKLSDIYQWLKEGVGLVHEFEKGDE

36. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 433, Application US/09617747

Sequence 433, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 433  
LENGTH: 10  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
HASAHASGRORHLSASTOIRNEPSPAMASLGQILFWSIIIIIIIIAGAILIIGFGISGRHSITVTYVASA  
|||||||  
QLEWSTISI  
X  
10

80 90  
GNIGEDGILSCFEPDIKLS

37. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 432, Application US/09617747

Sequence 432, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 432  
LENGTH: 10  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

230 240 250 260 270 280  
LNSENVTKMYVSVLVNTIINNYSCMIENDAKATGDIKVTSEIKRRSHLOLNSKASLCVSSFFAISWAL  
|||||||  
LOLLNSKASL  
X  
10

300  
LPLSPYMLK

38. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 430, Application US/09617747

Sequence 430, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

Sequence 418, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 418  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0  
230 240 250 260 270 280 X 300  
SENTMKVSVLYVNTINNTSCMIENDIAKATGDIKYESEIKRSHLQLLNKSKASLCVSSFFAISMALLP  
|||||  
LNLSKASLCV  
X  
10

LSPYIMLTK

47. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 417, Application US/09617747

Sequence 417, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 417  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0  
10 20 30 X 50 60 70  
HASAHASRQQLHASTQIRWEPSPAMASLGQILFWSIISIIIIILAGAILIIGFISGRHSITVTTVASA  
|||||  
SLGQILFWSI  
X  
10

80  
GNIGEDGILCTFEPDI

48. US-09-636-801-392 (1-309)  
US-09-617-747-41 Sequence 416, Application US/09617747

Sequence 416, Application US/09617747  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 416  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
Residue Identity = 100% Matches = 10 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0  
40 50 60 70 80 90 X 110  
ISIIIIAGAILIIGFISGRHSITVTTVASAGNIGEDGILCTFEPDIKSLDIVIOMLKEGVGLVHEPK  
|||||  
KLSDIVIOML  
X  
10

120 130 140  
EGKDELSQDEMFRCRTAVFADQVTVGNASLRLKNVQL

49. US-09-636-801-392 (1-309)  
US-09-617-747-39 Sequence 390, Application US/09617747

Sequence 390, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 390  
LENGTH: 438  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 51 Significance = -0.22  
Residue Identity = 20% Matches = 22 Mismatches = 58  
Gaps = 21 Conservative Substitutions = 9

EDALNQLFRNSISYSDCOVSTPRSRVPHHHTGVDSLNFSPLARVRVAIYEELFRMTNGTOLQNTT  
290 300 310 320 330 X 340 350  
HASAHA-----SGRQRO---  
|||||

APPLICANT: Fling, Steven P.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Fanger, Gary Richard  
 APPLICANT: Reed, Steven G.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.462C3  
 CURRENT APPLICATION NUMBER: US/09/617,747  
 CURRENT FILING DATE: 2000-07-17  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 424  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
 Residue Identity = 100% Matches = 10 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 190  
 MGRGRTAVADQVYVGNASLRKNVQLTGATYKCYITISKGKGNANLEKYGAFSPMEVNDYNASSETLR  
 ||||||||  
 KTGAFSMPEV  
 X 10

200 210 220 230  
 CEAPRRFPQPTVYMASQVDOGANFSEVNTSELNSEN

43. US-09-636-801-392 (1-309)  
 US-09-617-747-42 Sequence 423, Application US/09617747

Sequence 423, Application US/09617747  
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: King, Gordon E.  
 APPLICANT: Algate, Paul A.  
 APPLICANT: Fling, Steven P.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Fanger, Gary Richard  
 APPLICANT: Reed, Steven G.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.462C3  
 CURRENT APPLICATION NUMBER: US/09/617,747  
 CURRENT FILING DATE: 2000-07-17  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 423  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
 Residue Identity = 100% Matches = 10 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

210 220 230 240 250 X 270  
 PGPVYMASQVDOGANFSEVNTSELNSENVTMKVSVLYNVTINNYSCTMIENDIAKATGDIKYTESEIK  
 ||||||||  
 CMIENDIAKA  
 X 10

280 290 300  
 RRSHTQLNSKASLCVSSFFAISWALLPLSPYMLK

44. US-09-636-801-392 (1-309)  
 US-09-617-747-42 Sequence 421, Application US/09617747  
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: King, Gordon E.  
 APPLICANT: Algate, Paul A.  
 APPLICANT: Fling, Steven P.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Fanger, Gary Richard  
 APPLICANT: Reed, Steven G.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.462C3  
 CURRENT APPLICATION NUMBER: US/09/617,747  
 CURRENT FILING DATE: 2000-07-17  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 421  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
 Residue Identity = 100% Matches = 10 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
 HASAHASGRORLSASTQIRWEPSPAMASLGQILFWSTISITIIILAGATLITGFGISGRHSITVTYVASA  
 ||||||||  
 ILFWSTISIT  
 X 10

80 90  
 GNIGEDGILSCFREPDIKLSLD

45. US-09-636-801-392 (1-309)  
 US-09-617-747-41 Sequence 419, Application US/09617747

Sequence 419, Application US/09617747  
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: King, Gordon E.  
 APPLICANT: Algate, Paul A.  
 APPLICANT: Fling, Steven P.  
 APPLICANT: Retter, Marc W.  
 APPLICANT: Fanger, Gary Richard  
 APPLICANT: Reed, Steven G.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 FILE REFERENCE: 210121.462C3  
 CURRENT APPLICATION NUMBER: US/09/617,747  
 CURRENT FILING DATE: 2000-07-17  
 NUMBER OF SEQ ID NOS: 455  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 419  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22  
 Residue Identity = 100% Matches = 10 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300  
 KVVSVLYNVTINNYSCTMIENDIAKATGDIKYTESEIKRRSHQLNSKASLCVSSFFAISWALLPLSPYLM  
 ||||||||  
 SLCVSSFFAI  
 X 10

46. US-09-636-801-392 (1-309)  
 US-09-617-747-41 Sequence 418, Application US/09617747  
 LK

US-09-617-747-45 Sequence 454, Application US/09617747

Sequence 454, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 454  
LENGTH: 9  
TYPE: prt  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

90 100 110 120 130 140 150  
EPDIKSDIYQWLKEGYLVHFEKSGKDELSDQENKGRGTAVFADQVVGASLRLKNVQLTDAGTYKC  
|||||  
IVGNASLRL  
X X X

160 170 180 190  
YIITSKGGKGNANLEKTKGASMPENVNDYNASSETLR

54. US-09-636-801-392 (1-309)  
US-09-617-747-45 Sequence 453, Application US/09617747

Sequence 453, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 453  
LENGTH: 9  
TYPE: prt  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

40 50 60 70 80 90 100  
QILFWSIISIIILAGALAILIGFISGRHSITVTYVASAGNIGEDGILSTFEPDIKLSDIYQWLKEGYL  
|||||  
CTFEPDIKL  
X X X

110 120 130 140  
GLVHFEKSGKDELSDQENKGRGTAVFADQVVGAS

55. US-09-636-801-392 (1-309)  
US-09-617-747-45 Sequence 452, Application US/09617747

Sequence 452, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 452  
LENGTH: 9  
TYPE: prt  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
HASAHASGRQRLHSASTQIMWEPSPAMASLGQILFWSIISIIILAGALAILIGFISGRHSITVTYVASA  
|||||  
IALIIGFGI  
X X X

80 90 100  
GNIGEDGILSTFEPDIKLSDIYQWLKEGYLVH

56. US-09-636-801-392 (1-309)  
US-09-617-747-45 Sequence 451, Application US/09617747

Sequence 451, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 451  
LENGTH: 9  
TYPE: prt  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
HASAHASGRQRLHSASTQIMWEPSPAMASLGQILFWSIISIIILAGALAILIGFISGRHSITVTYVASA  
|||||  
SLGQILFWS  
X X X

53. US-09-636-801-392 (1-309)

190 200 210 220 230 X 240 250  
VNVYDMSSEFLRCEAPRWFPQPTVYMASQVQGANFSEVNTSELSNVTAKVYSLVNTNTNTYSCM  
|||||  
NVTMKVSV X  
X

260 270 280 290  
IENDIAKATGDIKVTSESEIKRRSHQLNSKASLCVS

61. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 443, Application US/09617747

Sequence 443, Application US/09617747  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 443  
LENGTH: 9  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 X 60 70  
HASAHASGRQRLHSASTQIMWSPSPAMASIGQLFWISITIIILACAIALLIGFGISGRHSITVTVASA  
|||||  
IILAGAIL X  
X

80 90 100  
GNIGEDGILSCTFEPDILSDIVIQWLKEG

62. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 441, Application US/09617747

Sequence 441, Application US/09617747  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 441  
LENGTH: 9  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 X 60 70  
HASAHASGRQRLHSASTQIMWSPSPAMASIGQLFWISITIIILACAIALLIGFGISGRHSITVTVASA  
|||||  
IILAGAILI X  
X

63. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 440, Application US/09617747

Sequence 440, Application US/09617747  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 440  
LENGTH: 9  
TYPE: PRF  
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24  
Residue Identity = 100% Matches = 9 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

190 200 210 220 230 X 240 X 250  
YNASSETLRCEAPRWFPQPTVYMASQVQGANFSEVNTSELSNVTAKVYSLVNTNTNTYSCMIEND  
|||||  
KVSVLYTV X  
X

260 270 280 290  
IAKATGDIKVTSESEIKRRSHQLNSKASLCVSSFFA

64. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 439, Application US/09617747

Sequence 439, Application US/09617747  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 439  
LENGTH: 9

80  
GNIGEDGILSCFEPD

57. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 448, Application US/09617747

Sequence 448, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Flinn, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 448  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	-	9	Optimized Score	-	9	Significance	-	-0.24
Residue Identity	-	100%	Matches	-	9	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	9		-	0

230 240 250 260 270 280 290 300  
SENWTKVSVLVNTYNTYSCMIENDIAKATGDIKTESEIKRRSHQLNLSKASLCVSSFFALSWALLP  
|||||  
LNLSKASLC  
X X X

LSPLYMLK

58. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 446, Application US/09617747

Sequence 446, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Flinn, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 446  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	-	9	Optimized Score	-	9	Significance	-	-0.24
Residue Identity	-	100%	Matches	-	9	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	9		-	0

80 90 100 110 120 130 140 150  
GLSCFEPDILKSDIVIQMLKEGVGLVHERKEGDELSEODEMRGRTAVFADQVIYGNASLRKNQVLT

160 170 180  
DACTYKCYIITSKGNANLEKYGAFSMEPVNDYN  
|||||  
AVFADQVIV  
X X

59. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 445, Application US/09617747

Sequence 445, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Flinn, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 445  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	-	9	Optimized Score	-	9	Significance	-	-0.24
Residue Identity	-	100%	Matches	-	9	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	9		-	0

80 90 100 110 120 X 130 140  
AGNIGEDGILSCFEPDILKSDIVIQMLKEGVGLVHERKEGDELSEODEMRGRTAVFADQVIYGNASLR  
|||||  
EMFRGRTAV  
X X

150 160 170 180  
LKNVQLDAGTYKCYIITSKGNANLEKYGAFSMP

60. US-09-636-801-392 (1-309)  
US-09-617-747-44 Sequence 444, Application US/09617747

Sequence 444, Application US/09617747

GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Flinn, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 444  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score	-	9	Optimized Score	-	9	Significance	-	-0.24
Residue Identity	-	100%	Matches	-	9	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	9		-	0





TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24  
Residue Identity - 100% Matches - 9 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

230 240 250 260 270 280 290 300  
NSENTMKVSVLYNTINTNTYSCHIENDIAKATGDIKYTESEIKRRSHLQLLNKSKASLCVSSFFAISWALL  
|||||  
QLNKSASL  
X X

PLSPYLMLK

65. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 438, Application US/09617747

Sequence 438, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 438

LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24  
Residue Identity - 100% Matches - 9 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

HASAHASGRQLHSASTQIRWEPSPAMASLQILFWSIISIIIIILAGAILILGIGISGRSITVTIVASA  
|||||  
ILFWSIISI  
X X

80 90  
GNIGEDGILSTCFEPDIKLS

66. US-09-636-801-392 (1-309)  
US-09-617-747-43 Sequence 437, Application US/09617747

Sequence 437, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 437  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24  
Residue Identity - 100% Matches - 9 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

240 250 260 270 280 290 300  
KVSVLYNTINTNTYSCHIENDIAKATGDIKYTESEIKRRSHLQLLNKSKASLCVSSFFAISWALLPLSPYLK  
|||||  
SLCVSSFFA  
X X

LK

67. US-09-636-801-392 (1-309)  
US-09-617-747-42 Sequence 420, Application US/09617747

Sequence 420, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3  
CURRENT APPLICATION NUMBER: US/09/617,747  
CURRENT FILING DATE: 2000-07-17  
NUMBER OF SEQ ID NOS: 455  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 420

LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24  
Residue Identity - 100% Matches - 10 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

190 200 210 220 230 240 250 260  
SETLRCEAPRWFPQPTVWASQVDGANSFSEVNTSEFLNSENVTKVSVLYNTINTNTYSCHIENDIAKA  
|||||  
VLXNTINTNT  
X 10

270 280 290  
TGDIKYTESEIKRRSHLQLLNKSKASLCVSSFFAISWALL

68. US-09-636-801-392 (1-309)  
US-09-617-747-38 Sequence 388, Application US/09617747

Sequence 388, Application US/09617747  
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
APPLICANT: Fling, Steven P.  
APPLICANT: Retter, Marc W.  
APPLICANT: Fanger, Gary Richard  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.462C3



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> 0 <  
01 10 Intelligenetics  
> 0 <

FastDB : Fast Pairwise Comparison of Sequences  
Release 5.4

Results file US09404879.res made by sdavid on Mon 23 Jul 101 13:41:48-PDT.

Query sequence being compared: US-09-636-801-392 (1-309)  
Number of sequences searched: 6  
Number of scores above cutoff: 6

Results of the initial comparison of US-09-636-801-392 (1-309) with:  
File : US09404879A.pep

100-  
N 50-  
U 50-  
M 50-  
B 50-  
E 50-  
R 50-  
O 10-  
F 10-  
S 10-  
E 5-  
U 5-  
O 5-  
U 5-  
E 5-  
N 5-  
C 5-  
S 5-  
SCORE 0 34 69 103 137 172 206 240 275 309  
STDEV 0 0 0 0 0 0 0 0 0 0

PARAMETERS  
Similarity matrix PAM-150  
Threshold level of sim. 16%  
Mismatch penalty 1  
Gap penalty 1.00  
Gap size penalty 0.05  
Cutoff score 0  
Randomization group 0

SEARCH STATISTICS  
Scores: Mean 104 Median 11 Standard Deviation 148.07  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 3548  
Number of sequences searched: 6  
Number of scores above cutoff: 6

The scores below are sorted by initial score.  
Significance is calculated based on initial score.  
A 100% identical sequence to the query sequence was found:

Sequence Name Description Init. Opt. Length Score Score Sig. Frame

1. US-09-404-879A-3 Sequence 392, Application 309 309 309 1.38 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Score	Sig. Frame
2. US-09-404-879A-3 Sequence 393, Application 282	**** 1 standard deviation above mean ****	282	282	282	1.20	0
3. US-09-404-879A-3 Sequence 390, Application 438	*** 0 standard deviation from mean ***	438	10	51	-0.63	0
4. US-09-404-879A-3 Sequence 389, Application 833		833	10	51	-0.63	0
5. US-09-404-879A-3 Sequence 312, Application 914		914	10	51	-0.63	0
6. US-09-404-879A-3 Sequence 388, Application 772		772	7	153	-0.66	0

1. US-09-636-801-392 (1-309)  
US-09-404-879A-3 Sequence 392, Application US/09404879A

Sequence 392, Application US/09404879A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404,879A  
CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 392  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Homo sapiens

Initial Score = 309 Optimized Score = 309 Significance = 1.38  
Residue Identity = 100% Matches = 309 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
HASAHSGROROLHSASTOIRWEPSPAMASLGQILFWSIIIIILAGATALLIGFISGRHSITVTVASA  
HASAHSGROROLHSASTOIRWEPSPAMASLGQILFWSIIIIILAGATALLIGFISGRHSITVTVASA  
X 10 20 30 40 50 60 70  
GNIGEDGIIISCTFEPIKISDIYIOWLKEGYLVHFEKGRKDELSPQDEMERGRVAFVADQYIVGNASIRL  
GNIGEDGIIISCTFEPIKISDIYIOWLKEGYLVHFEKGRKDELSPQDEMERGRVAFVADQYIVGNASIRL  
X 80 90 100 110 120 130 140  
KNVQLPDAGTYKCYIITISKSGNANLEFKTGAFSPMPVNDVYNASSITLRCAPRPFPOPTVYMAOYDGA  
KNVQLPDAGTYKCYIITISKSGNANLEFKTGAFSPMPVNDVYNASSITLRCAPRPFPOPTVYMAOYDGA  
X 150 160 170 180 190 200 210  
NFESEVNTSFELSENVTAKVSVLYVNTINNTYSCMIENDIKAKGDIYVTSSEIKRSHLOLLNSKASLC  
NFESEVNTSFELSENVTAKVSVLYVNTINNTYSCMIENDIKAKGDIYVTSSEIKRSHLOLLNSKASLC  
X 220 230 240 250 260 270 280  
VSSFFAISMALPLSPYLMK  
VSSFFAISMALPLSPYLMK  
X 290 300  
VSSFFAISMALPLSPYLMK  
VSSFFAISMALPLSPYLMK  
X 290 300

2. US-09-636-801-392 (1-309)

US-09-404-879A-3 Sequence 393, Application US/09404879A

Sequence 393, Application US/09404879A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 393

LENGTH: 282

TYPE: PR

ORGANISM: Homo sapiens  
Initial Score - 282 Optimized Score - 282 Significance - 1.20  
Residue Identity - 100% Matches - 282 Mismatches - 0  
Gaps - 0 Conservative Substitutions - 0

HASAHASGROQLHSASTQIRMEPSPAMASLGQILFWSTIIIIIIAGATLIIIGTSGRHSITVTYASA  
|||||  
MASLGQILFWSTIIIIIIAGATLIIIGTSGRHSITVTYASA  
X  
10 20 30 40 50 60 70

GNIGEDGILSCFEEDIKLSDIVIQMLKEGVGLVHEFEKDELSDEDEMRGTAFAVDQVYGNASLRL  
|||||  
GNIGEDGILSCFEEDIKLSDIVIQMLKEGVGLVHEFEKDELSDEDEMRGTAFAVDQVYGNASLRL  
50 60 70 80 90 100 110

150 160 170 180 190 200 210  
KNQVLTLDAGTYACYYITTSKGNANLEKKTGAFSMPEVVDVNASSETLRCAAPWFPPOPTVYMASOVDGA  
|||||  
KNQVLTLDAGTYACYYITTSKGNANLEKKTGAFSMPEVVDVNASSETLRCAAPWFPPOPTVYMASOVDGA  
120 130 140 150 160 170 180

220 230 240 250 260 270 280  
NFSEVSNTSFELNSENVTKMYVSVLYNTYNTYSCMIENDIAKATGDIKTESIKRSHLOLNSKASLC  
|||||  
NFSEVSNTSFELNSENVTKMYVSVLYNTYNTYSCMIENDIAKATGDIKTESIKRSHLOLNSKASLC  
190 200 210 220 230 240 250 260

290 300 X  
VSSFFAISMALPLSPYMLK  
|||||  
VSSFFAISMALPLSPYMLK  
270 280 X

3. US-09-636-801-392 (1-309)  
US-09-404-879A-3 Sequence 390, Application US/09404879A

Sequence 390, Application US/09404879A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 390

LENGTH: 438

TYPE: PR

ORGANISM: Homo sapiens

Initial Score - 10 Optimized Score - 51 Significance - -0.63  
Residue Identity - 20% Matches - 22 Mismatches - 58  
Gaps - 21 Conservative Substitutions - 9

EDALNQLFRNSSIKSYFSDCOVSTFRSVPNRRHHTGVDSLGNFSPILARRVDRAVAIYEFLRMTNGTOLNFT  
250 300 310 320 330 340 350  
X  
HASAHA-----SGRORO---  
|||||

20 30 40 50 60 70 80  
LHASASTQIR---WEPSPAMASLGQILFWSTIIIIIIAGATLIIIGTSGRHSITVTYASAGNIGEDGIL  
|||||  
LDRSSVLVDGYFPNRRNEPLTGNSDLPFAVAV--ILIGLAGLGLITCL-ICG---VLVYTRRRRKEGEYVVOQ  
360 370 380 390 400 410 420

90 X 100 110 120 130 140  
SCT--FEEDIKLSDIVIQMLKEGVGLVHEFEKDELSDEDEMRGTAFAVDQVYGNASLRLK  
|||||  
OCPGYOSHLDLEDIQ  
X  
430

4. US-09-636-801-392 (1-309)  
US-09-404-879A-3 Sequence 389, Application US/09404879A

Sequence 389, Application US/09404879A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.462C2  
CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 389

LENGTH: 833

TYPE: PR

ORGANISM: Homo sapiens

Initial Score - 10 Optimized Score - 51 Significance - -0.63  
Residue Identity - 20% Matches - 22 Mismatches - 58  
Gaps - 21 Conservative Substitutions - 9

EDALNQLFRNSSIKSYFSDCOVSTFRSVPNRRHHTGVDSLGNFSPILARRVDRAVAIYEFLRMTNGTOLNFT  
680 690 700 710 720 730 740 750  
X  
HASAHA-----SGRORO---  
|||||

20 30 40 50 60 70 80  
LHASASTQIR---WEPSPAMASLGQILFWSTIIIIIIAGATLIIIGTSGRHSITVTYASAGNIGEDGIL  
|||||  
LDRSSVLVDGYFPNRRNEPLTGNSDLPFAVAV--ILIGLAGLGLITCL-ICG---VLVYTRRRRKEGEYVVOQ  
760 770 780 790 800 810

90 X 100 110 120 130 140  
SCT--FEEDIKLSDIVIQMLKEGVGLVHEFEKDELSDEDEMRGTAFAVDQVYGNASLRLK  
|||||  
OCPGYOSHLDLEDIQ  
X  
820 830 X

5. US-09-636-801-392 (1-309)  
US-09-404-879A-3 Sequence 312, Application US/09404879A

Sequence 312, Application US/09404879A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.  
APPLICANT: Algate, Paul A.



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RP SEQUENCE OF 39-487 FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=96125722; PubMed=8541302;  
 RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;  
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin  
 RT specifically associates with a 150-kDa protein of mammary epithelial  
 RT cells and milk fat globule membrane.";  
 RL Biochim. Biophys. Acta 1245:285-292(1995).  
 CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT  
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE  
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA  
 CC MEMBRANE (BY SIMILARITY).  
 CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN  
 CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF  
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.  
 CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).  
 CC  
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 CC  
 CC EMBL: U67065; AAB51034.1; -  
 CC EMBL: S80642; AAB35893.1; -  
 CC MGD: MGI:103118; Btn.  
 CC InterPro: IPR000107; -  
 CC InterPro: IPR003006; -  
 CC Pfam: PF00622; SPRY; 1.  
 CC Pfam: PF00047; 1g; 1.  
 CC Transmembrane: Glycoprotein; Immunoglobulin domain; Signal.  
 CC  
 CC SIGNAL 1 26  
 CC FT CHAIN 27 524  
 CC FT DOMAIN 27 247  
 CC FT TRANSMEM 248 268  
 CC FT DOMAIN 269 524  
 CC FT CARBOHYD 56 56  
 CC FT CARBOHYD 216 216  
 CC FT CONFLICT 46 46  
 CC FT CONFLICT 117 117  
 CC FT CONFLICT 191 191  
 CC FT CONFLICT 210 210  
 CC FT CONFLICT 363 363  
 CC FT CONFLICT 408 408  
 CC FT CONFLICT 413 414  
 CC FT CONFLICT 420 423  
 CC FT CONFLICT 492 509  
 CC  
 CC SEQUENCE 524 AA; 58406 MW; 333F4D52C7704480 CRC64;  
 SO  
 Query Match 11.3%; Score 178.5; DB 1; Length 524;  
 Best Local Similarity 22.7%; Pred. No. 4e-07;  
 Matches 45; Conservative 51; Mismatches 93; Indels 9; Gaps 4;

OY 251 SCMIENDIAKATGDIKYT 268  
 DB 218 SCCTONILLGCKEVELS 235  
 RESULT 4  
 ID CD80\_RABIT STANDARD; PRT; 299 AA.  
 AC P42070;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD80 PRECURSOR (ACTIVATION B7-1  
 DE ANTIGEN).  
 GN CD80.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B/J x CHB; HM;  
 RX MEDLINE=95369849; PubMed=7642234;  
 RA Isono T., Seto A.;  
 RT "Cloning and sequencing of the rabbit gene encoding T-cell  
 RT costimulatory molecules.";  
 RL Immunogenetics 42:217-220(1995).  
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T  
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE  
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS  
 CC RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC  
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 CC  
 CC EMBL: D49843; BAA08643.1; -  
 CC InterPro: IPR003006; -  
 CC Pfam: PF00047; 1g; 1.  
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;  
 CC Receptor.  
 CC  
 CC SIGNAL 1 32  
 CC FT CHAIN 33 299  
 CC FT DOMAIN 33 243  
 CC FT TRANSMEM 244 264  
 CC FT DOMAIN 265 299  
 CC FT DOMAIN 42 122  
 CC FT DOMAIN 154 222  
 CC FT DISULFID 49 115  
 CC FT DISULFID 161 215  
 CC FT CARBOHYD 52 52  
 CC FT CARBOHYD 88 88  
 CC FT CARBOHYD 97 97  
 CC FT CARBOHYD 122 122  
 CC FT CARBOHYD 185 185  
 CC FT CARBOHYD 206 206  
 CC FT CARBOHYD 210 210  
 CC  
 CC SEQUENCE 299 AA; 33513 MW; 6744223E5CC91DE0 CRC64;  
 SO  
 Query Match 10.4%; Score 163.5; DB 1; Length 299;  
 Best Local Similarity 25.3%; Pred. No. 3.1e-06;  
 Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

DB 19 LCLLALAG---LHSSSGIS-----QVTK-----SVKEMALSCDTNISTDLAKMRITW 65  
QY 99 LKEG---VLGLVHEFEKDELSQDEMERGRTRAVFADQYIVGNASRLKNNVOLTADGTYK 156  
DB 66 QKQDQMWIIL---SGQVEWPE---YKNRT--FPD--IINNLSMILALSLSKGTYT 114  
QY 157 CYITTSKKGANLNEYKGA-----FSMEPV---NVDYNASSETLRCEAPRNPPOPT 205  
DB 115 C-VVQKNENSGFRRHRLTSVLTSLIRADPPVPSTIDIGHDDPVN--KRIRCSASGGFPEPR 171  
QY 206 VYMASQVQGANFSEVSNTPSELSNENTMKVSVL-VNVTINNNTYSCMIENDIAKAGD 264  
DB 172 LAM---MEDGEPLNAV-NITYDQDLDTLEYSVSSELDENVNHNHSIVCLIK-----YGE 221  
QY 265 IKVTE---SEIKRRSHQLNLNSKASLCVSSPFAISMAILPLSPYLM 308  
DB 222 LVSQIFPMWKRKQEPIDQLP-----FWYIIPVSGALVL 256  
RESULT 5  
MOG\_RAT  
ID MOG\_RAT STANDARD: PRT: 245 AA.  
AC 063345:  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.  
GN MOG.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
[1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=93085763; PubMed=1453482;  
RA Gardiner M.V., Amiguet P., Linington C., Mathieu J.-M.;  
RT "Myelin/oligodendrocyte glycoprotein is a unique member of the  
RT immunoglobulin superfamily";  
RL J. Neurosci. Res. 33:177-187(1992).  
RN [2]  
RP SEQUENCE OF 28-245 FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93376728; PubMed=8367453;  
RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,  
RA Portarotti P., Roessel N., Mather I.H., Artzt K., Lindahl K.F.,  
RA Dautigny A.;  
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the  
RT immunoglobulin superfamily encoded within the major  
RT histocompatibility complex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).  
RN [3]  
RP STRUCTURE BY NMR OF 62-82.  
RX MEDLINE=97354172; PubMed=9210466;  
RA Alouf-Abo S., Wilson J.C., Bernard C.C.A., von Izstein M.;  
RT "A confocal study of the human and rat cephalic myelin  
RT oligodendrocyte glycoprotein peptides 35-55.";  
RL Eur. J. Biochem. 246:59-70(1997).  
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN  
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-  
CC CELL COMMUNICATION.  
CC -1- SUBUNIT: MAY FORM HOMODIMERS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS  
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC  
CC MEMBRANES.  
CC -1- DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED  
CC BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOD OF  
CC ACTIVE MYELINATION.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE V-LIKE DOMAIN. BELONGS TO THE RTN/MOG SUBFAMILY.  
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)  
CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).

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CC -----  
CC DR EMBL: M99485; AAA41628.1; -;  
CC DR EMBL: L21995; AAF74786.1; -;  
CC DR InterPro: IPR003006; -;  
CC Pfam: PF00047; 1g.1;  
CC Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.  
CC SIGNAL 1 27  
CC CHAIN 28 245 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.  
CC DOMAIN 28 155 EXTRACELLULAR (POTENTIAL).  
CC TRANSMEM 156 176 POTENTIAL.  
CC DOMAIN 177 208 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 209 229 POTENTIAL.  
CC DOMAIN 230 245 EXTRACELLULAR (POTENTIAL).  
CC DOMAIN 44 132 IG-LIKE V-TYPE DOMAIN.  
CC DISULFID 51 125 POTENTIAL.  
CC CARBOHYD 58 58 N-LINKED (GLCNAc. ...) (POTENTIAL).  
CC SEQUENCE 245 AA; 27881 MW; C97F8AD60D6A32B4 CRC64;  
SQ  
Query Match 9.7%; Score 152; DB 1; Length 245;  
Best Local Similarity 26.2%; Pred. No. 2e-05; Mismatches 55; Indels 24; Gaps 5;  
Matches 39; Conservative 31;  
QY 37 WS-----IISIIIL-----AGAILIIGISGRHSITVTVASGNIGEDSLCT 84  
DB 5 WLSLSPCLSLILLQLQSRVAGQFR-VIGPG-----HPIRAL-----VEDAEALPCR 52  
QY 85 FEPDLKLSIVQLAKEVGLVHEFEKDELSQDEMERGRTRAVFADQYIVGNASRL 144  
DB 53 ISPGNAGMEGWYRSPFSRVHLRYNGKDDADQAEPRTELKESIGCKVALRI 112  
QY 145 KVVOLTDAQTYKCYITTSKKGANLNEYK 173  
DB 113 QVNRSDSGTYCFRRDHSYQDEAAVELK 141  
RESULT 6  
MOG\_MOUSE  
ID MOG\_MOUSE STANDARD: PRT: 246 AA.  
AC 061885; Q62003; F70364;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.  
GN MOG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=95130110; PubMed=7829100;  
RA Daubas P., Pham-Dinh D., Dautigny A.;  
RT "Structure and polymorphism of the mouse myelin/oligodendrocyte  
RT glycoprotein gene.";  
RL Genomics 23:36-41(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gardiner M.V., Mathieu J.M.;  
RT "Murine and human MOG are highly conserved: cDNA analysis.";  
RL Trans. Am. Soc. Neurochem. 24:234-234(1993).  
RN [3]  
RP SEQUENCE OF 29-246 FROM N.A.  
RC STRAIN=BAUB/C; TISSUE=Brain;

RX MEDLINE=93376728; PubMed=8367453;  
RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,  
RA Pontorotti P., Roeckel N., Mather I.H., Altzt K., Lindahl K.F.,  
RA Dautigny A.;  
RT "Myelin/Oligodendrocyte glycoprotein is a member of a subset of the  
RT immunoglobulin superfamily encoded within the major  
RT histocompatibility complex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).  
RN (4)  
RP SEQUENCE OF 29-54.  
RC STRAIN-BALB/C; TISSUE-Brain;  
RX MEDLINE=92218912; PubMed=1373175;  
RA Amiguet P., Gardiner M.V., Zanetta J.-P., Mathieu J.-M.;  
RT "Purification and partial structural and functional characterization  
RT of mouse myelin/oligodendrocyte glycoprotein.";  
RL J. Neurochem. 58:1676-1682(1992).  
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN  
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-  
CC CELL COMMUNICATION.  
CC -1- SUBUNIT: MAY FORM HOMODIMERS.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS  
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC  
CC MEMBRANES.  
CC -1- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND  
CC QUACKING DYSMYELINATING MUTANT MICE.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.  
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)  
CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).  
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CC -----  
DR EMBL: L29503; AAC42023.1; -;  
DR EMBL: L29498; AAC42023.1; JOINED.  
DR EMBL: L29500; AAC42023.1; JOINED.  
DR EMBL: L29501; AAC42023.1; JOINED.  
DR EMBL: L29499; AAC42023.1; JOINED.  
DR EMBL: L29502; AAC42023.1; JOINED.  
DR EMBL: U64572; AAB08096.1; -;  
DR EMBL: L20942; AAA03180.1; -;  
DR MGD: MGI:97435; Moq.  
DR InterPro: IPR003006; -;  
DR Pfam: PF00047; Ig; 1.  
DR Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.  
FT CHAIN 1 28  
FT STGNL 28  
FT DOMAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.  
FT TRANSMEM 157 177 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 178 209 POTENTIAL.  
FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 231 246 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 45 133 IG-LIKE V-TYPE DOMAIN.  
FT DISULFID 52 126 POTENTIAL.  
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CONFLICT 21 21 L-> L (IN REF. 2).  
FT CONFLICT 32 32 R-> G (IN REF. 4).  
FT CONFLICT 95 95 G-> E (IN REF. 3).  
FT CONFLICT 169 169 P-> S (IN REF. 2).  
SQ SEQUENCE 246 AA; 28271 MW; 1F1A8AAAD5CF889 CRC64;

Query Match 9.6%; Score 150.5; DB 1; Length 246;  
Best Local Similarity 23.8%; Pred. No. 2.7e-05;  
Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;  
QY 37 WS-----IISIIIIAGALALIIGFISGRHSITVTVAASAGNIGDGLISCFEPDIK 90

DB 5 WSFWPSCPLSLILL-----LQLSCTYACOFRTYICGYPIRALYGVGBEALPCISCKN 59  
QY 91 LSDIVQMLKEGVGLVHERKEGKDELSEDEMERGRTAVFADOVIVGNLSRLKNVLT 150  
DB 60 ATGMEVGMSPFSRVRVHLVRNGKDQDAEQAPRYGRTELLKRTISGKVTLRIONRFS 119  
QY 151 DACTYKCIITTSKSGKANLEFK 173  
DB 120 DEGGYTCFPRDHSYQEBAMELK 142  
RESULT 7  
ID CD86\_HUMAN STANDARD; PRT; 329 AA.  
AC P42081; Q13655;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2  
DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).  
GN CD86 OR CD28LG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94053735; PubMed=7694363;  
RA Freeman G.J., Gribben J.G., Boussetios V.A., Ng J.W.,  
RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;  
RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T  
RT cell proliferation.";  
RL Science 262:909-911(1993).  
RN [2]  
RP SEQUENCE OF 7-329 FROM N.A.  
RX MEDLINE=94050123; PubMed=7694153;  
RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,  
RA Lanier L.L., Somoza C.;  
RT "B70 antigen is a second ligand for CTLA-4 and CD28.";  
RL Nature 366:76-79(1993).  
RN [3]  
RP SEQUENCE OF 7-329 FROM N.A.  
RC TISSUE=Forrestin;  
RX MEDLINE=95331831; PubMed=7541777;  
RA Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,  
RA Green N.R., Gray G.S.;  
RT "Genomic organization of the gene coding for the costimulatory human  
RT B-1 lymphocyte antigen B7-2 (CD86)."  
RL Immunogenetics 42:85-89(1995).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=95088403; PubMed=7527824;  
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,  
RA Okumura K., Ito D., Azuma M.;  
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T  
RT cell proliferation, cytokine production, and generation of CTL.";  
RN Immunol. 154:97-105(1995).  
RN [5]  
RP IDENTIFICATION AS CD86.  
RX MEDLINE=94348060; PubMed=7520767;  
RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,  
RA Nadler L.M., Wakasa H., Tedder T.F.;  
RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and  
RT activated B lymphocytes is the CD86 differentiation antigen.";  
RL Blood 84:1402-1407(1994).  
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY  
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY  
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,  
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T  
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND  
CC MONOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.  
CC -1- DATABASE: NAME=PROV: NOTE=CD guide CD86 entry:  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: L25259; AAA8389.1; -  
DR EMBL: U04343; AAB0314.1; -  
DR EMBL: U17722; AAA86473.1; -  
DR EMBL: U17717; AAA86473.1; JOINED.  
DR EMBL: U17718; AAA86473.1; JOINED.  
DR EMBL: U17719; AAA86473.1; JOINED.  
DR EMBL: U17721; AAA86473.1; JOINED.  
DR MIM: 601020; -  
DR InterPro: IPR000495; -  
DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
KW Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;  
Receptor.  
FT SIGNAL 1 23  
FT CHAIN 24 329  
FT DOMAIN 24 247  
FT TRANSMEM 248 268  
FT DOMAIN 269 329  
FT DOMAIN 33 117  
FT SWAIN 33 117  
FT DISULFED 149 225  
FT DISULFED 157 218  
FT CARBOHYD 33 33  
FT CARBOHYD 47 47  
FT CARBOHYD 135 135  
FT CARBOHYD 146 146  
FT CARBOHYD 154 154  
FT CARBOHYD 177 177  
FT CARBOHYD 192 192  
FT CARBOHYD 213 213  
FT CONFLICT 27 27  
SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;  
  
Query Match 9.48; Score 147.5; DB 1; Length 329;  
Best Local Similarity 23.48; Pred. No. 7e-05;  
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;  
  
QY 50 IALIGISGRHSITVTVAAGNIGEDGILCTF--EPDIKLSDIYOMLKEGVGLV 107  
DB 12 ILFVAFILSLGAPAKIQAAY-----FNETADLPFCFANSQNSLSLVEVFWDDQENL-VL 65  
QY 108 HEKKGKDELSEQDEMERGRTAVFADQYIVGASLRLKNVOLDAGTYKCYITTSKGG- 166  
DB 66 NEVYLGRKEDFSVHSGKRTSFSDS-----SWTLRLNLHLQIKDKGLQCILHHKKPTGM 120  
QY 167 ----NANLETKGA-FSMPEV-----NDYNASSEFLRCEAPRMFQPIYVMA5QVDOGAN 217  
DB 121 IRIHOMNSELVLANFSDPEIVPISITENYI-NLTCSSIHGYDEP----- 166  
QY 218 FSEVNTSFELNSENVNKKV-----VSILNVNTI-----NNTYSCMIEN 256  
DB 167 ----KKMSVLRTKNTSTIEYDQIMKSDQNTVELDVSTLSVSPDYTSNMTITCILET 222  
QY 257 DIAKATGDIKVTSEIKR--RSHLOLNS--KASLCVSSFFAISM 297  
DB 223 DKTRLLSPFSIELEDPPRPDHPIMWITAVLPTVITICWVFLILIM 268

RESULT 8  
ID CD86\_RABIT STANDARD: PRT; 330 AA.  
AC P42071;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2  
DE ANTIGEN).  
GN CD86.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B/J X CHB:HM;  
RX MEDLINE=95369849; PubMed=7642234;  
RA Isono T., Seto A.;  
RT "Cloning and sequencing of the rabbit gene encoding T-cell  
RT costimulatory molecules.";  
RL Immunogenetics 42:217-220(1995).  
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL  
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY  
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY  
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,  
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T  
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.  
CC -----  
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CC -----  
DR EMBL: D49842; BAA08642.1; -  
DR InterPro: IPR000495; -  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; T-cell; Glycoprotein; signal; Transmembrane;  
Receptor.  
FT SIGNAL 1 22  
FT CHAIN 23 330  
FT DOMAIN 23 247  
FT TRANSMEM 248 268  
FT DOMAIN 269 330  
FT DOMAIN 33 117  
FT SWAIN 33 117  
FT DISULFED 149 225  
FT DISULFED 157 218  
FT CARBOHYD 33 33  
FT CARBOHYD 47 47  
FT CARBOHYD 135 135  
FT CARBOHYD 146 146  
FT CARBOHYD 154 154  
FT CARBOHYD 177 177  
FT CARBOHYD 192 192  
FT CARBOHYD 213 213  
FT CONFLICT 27 27  
SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57E3EE1 CRC64;  
  
Query Match 9.48; Score 147.5; DB 1; Length 330;  
Best Local Similarity 24.08; Pred. No. 7.1e-05;  
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;  
  
QY 38 STIISIIILAGAILIGISGRHSITVTVAAGNIGEDGILCTF--EPDIKLSDIY 95  
DB 12 TVFVALLSLGASLRI-----QATNKTRADLPFCQFTNSQSRSLSELY 54



RA	Ablour- <i>do S.</i> , Wilson J.C., Bernard C.C.A., vonlitzstein M.;
RT	"A conformational study of the human and rat encephalitogenic myelin
RL	oligodendrocyte glycoprotein peptides 35-55.";
Eur. J. Biochem.	246:59-70(1997).
CC	-1 FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC	COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC	CELL COMMUNICATION.
CC	-1 SUBUNIT: MAY FORM HOMO- OR HETERODIMERS BETWEEN THE DIFFERENT
CC	ISOFORMS.
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (ISOFORMS ALPHA-1
CC	AND BETA-1); TYPE I MEMBRANE PROTEIN (OTHER ISOFORMS) (POTENTIAL).
CC	-1 ALTERNATIVE PRODUCTS: AT LEAST 9 ISOFORMS; ALPHA-1 (SHOWN HERE),
CC	-2, -3, -4, BETA-1, -2, -3, -4 AND A SHORT ISOFORM ARE PRODUCED BY
CC	ALTERNATIVE SPLICING. THE SHORT ISOFORM IS NOT FUNCTIONALLY
CC	ACTIVE, IT MAY BE EXPRESSED AT LOW LEVEL IN THE ADULT.
CC	-1 TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC	LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC	MEMBRANES.
CC	-1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC	ONE V-LIKE DOMAIN. BELONGS TO THE BIN/MOG SUPERFAMILY.
CC	-1 CAUTION: DO NOT CONFUSE MELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
CC	WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
CC	-----
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CC	the European Bioinformatics institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL: X74511; CAA52617.1; -
DR	EMBL: Z48051; CAA88109.1; -
DR	EMBL: U18840; AAC50361.1; -
DR	EMBL: U18843; AAC50362.1; -
DR	EMBL: U18798; AAC50876.1; -
DR	EMBL: U18799; AAC50877.1; -
DR	EMBL: U18800; AAB35670.1; -
DR	EMBL: U18801; AAC50878.1; -
DR	EMBL: U18803; AAC50879.1; -
DR	EMBL: U64564; AAB08088.1; -
DR	EMBL: U64565; AAB08089.1; -
DR	EMBL: U64566; AAB08090.1; -
DR	EMBL: U64567; AAB08091.1; -
DR	EMBL: U64568; AAB08092.1; -
DR	EMBL: U64569; AAB08093.1; -
DR	EMBL: U64570; AAB08094.1; ALT_SEQ.
DR	EMBL: U64571; AAB08095.1; ALT_SEQ.
DR	HSSP: O13740; KGC.
DR	MIM: 159465; -
DR	InterPro: IPR003006; -
DR	Pfam: PF00047; Ig_1.
KW	Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal;
KW	Alternative splicing.
FT	SIGNAL 1 29
FT	CHAIN 30 247 POTENTIAL.
FT	DOMAIN 30 154 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
FT	TRANSMEM 155 175 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 176 210 POTENTIAL.
FT	TRANSMEM 211 231 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 232 247 POTENTIAL.
FT	DOMAIN 242 247 EXTRACELLULAR (POTENTIAL).
FT	DISULFID 53 127 IG-LIKE V-TYPE DOMAIN.
FT	CARBOHYD 60 60 POTENTIAL.
FT	VARSPLIC 30 145 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	VARSPLIC 198 203 MISSING (IN ISOFORM ALPHA-4).
FT	VARSPLIC 204 247 DPHFR -> GKPRHV (IN SHORT ISOFORM).
FT	VARSPLIC 198 236 MISSING (IN SHORT ISOFORM).
FT	VARSPLIC 204 247 DPFLRVCWKITLFVTPVYLGPVLAVITLCNWLRRRIA
FT	VARSPLIC 198 236 -> ESFVLGVQVEPKPT (IN ISOFORM ALPHA-3
FT	VARSPLIC 198 236 AND ISOFORM BETA-3).
FT	VARSPLIC 198 236 MISSING (IN ISOFORM ALPHA-2 AND ISOFORM
FT	VARSPLIC 198 236 BETA-2).
FT	VARSPLIC 198 243 MISSING (IN ISOFORM BETA-4).

FT	VANSPPLIC	244	247	RNPE -> LEFTLEALSG (IN ISOFORM BETA-1, ISOFORM BETA-2, ISOFORM BETA-3 AND ISOFORM BETA-4).
FT	CONFLICT	171	171	V-> L (IN REF. 3).
FT	SEQUENCE	247 AA;	28179 MM;	847601FFE5997ABOC CRC64;
SQ				
	Query Match	9.1%;	Score 144;	DB 1; Length 247;
	Best Local Similarity	20.8%;	Pred. No. 9.1e-05;	
	Matches 49;	Conservative 39;	Mismatches 80;	Indels 68; Gaps 6;
OY	28 MASIGLIFWMSIISIIL-----AGAILGIGSIRHSITVTVASACNGED 78	:   :		:   :
Db	1 MASI SRPLPSCLCFLLILLLOVSSSAAGPRV-----IGRHRTRL-----VDDE 48	:	:	:
OY	79 GLISTFEPIKRLSDIVIQMLEGVGLVHEKEKGDELSEDFEMGRATAVFDQVIWG 138	:   :		:   :
Db	49 VELPERISPKNKATMEGWRRPERSRVYLHNRKGDDGDGAPEYRGRTTELLKAIEGG 108	:	:	:
OY	139 NASLFKLKVOLTDACTYCIIYTISKGNANLEIKTGAFSPEVNVDMASSETLRCAP 198	:   :		:   :
Db	109 KYTLRIKVRFRPSDEGEFCFFRDHSYQEAAE-----LKVEDP 147	:	:	:
OY	199 RWFPGPTVMNASQVDOGANSFVSNTSPELSENENTMKVASY-LYNVTINTNYSCM 253	:   :		:   :
Db	148 FYWSPGYL-----VLNAVLPYLLLIQTIVGLVFIDL 178	:	:	:
RESULT	11			
CD86_MOUSE		STANDARD:	PRT:	309 AA.
ID	CD86_MOUSE			
AC	P42082			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2			
DE	ANTIGEN) (EARLY T CELL COSTIMULATORY MOLECULE-1) (ETC-1).			
CN	CD86.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCHI_TaxID=10090;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=94065585; PubMed=7504059;			
RA	Freeman G.J., Borriello F., Hodess R.J., Reiser H., Gibben J.G.,			
RA	Ng J.W., Kim J., Goldberg J.M., Hatcock K., Laszlo G., Lombard L.A.,			
RA	Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;			
RT	"Murine B7-2, an alternative CTLA4 counter-receptor that costimulates			
RT	T cell proliferation and interleukin 2 production.";			
RL	J. Exp. Med. 178:2185-2192(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=129;			
KX	MEDLINE=96094437; PubMed=7499829;			
RA	Borriello F., Oliveira J., Freeman G.J., Nadler L.M., Sharpe A.H.;			
RT	"Differential expression of alternate mb7-2 transcripts.";			
RL	J. Immunol. 155:5490-5497(1995).			
RN	[3]			
RP	SEQUENCE OF 7-309 FROM N.A.			
KX	MEDLINE=94230971; PubMed=7513726;			
RA	Chen C., Gault A., Shen L., Nabavi N.;			
RT	"Molecular cloning and expression of early T cell costimulatory			
RT	molecule-1 and its characterization as B7-2 molecule.";			
RL	J. Immunol. 152:4929-4936(1994).			
CC	- - FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL			
CC	FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY			
CC	BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY			
CC	EVENES OF T CELL ACTIVATION AND COSIGNALMENT OF NAIVE T CELLS,			
CC	SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T			
CC	CELLS WITHIN 24 HOURS AFTER ACTIVATION.			
CC	- - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- - TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.			

[illegible]







RA		MEDLINE=86140120; PubMed=3512556,
RX	Rougon G., Marshak D.R.;	"Structural and immunological characterization of the amino-terminal domain of mammalian neural cell adhesion molecules.";
RT	J. Biol. Chem.	261:3396-3401(1986).
RL	[3]	
RN	IDENTIFICATION AS N-CAM.	
RP	MEDLINE=9211748; PubMed=1765159;	
RA	Premont R.T.;	
RT	"A bovine brain cDNA purported to encode calmodulin-insensitive adenyllyl cyclase has extensive identity with neural cell adhesion molecules (N-CAMs).";	
RT	FEBS Lett.	295:230-231(1991).
CC	-1 FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC.	
CC	-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1 ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.	
CC	-1 SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.	
CC	-1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	
CC	-1 CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A CALMODULIN-INDEPENDENT ADENYLYL CYCLASE.	
CC	-----	
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CC	EMBL; X16451; CA34470.1; .	
DR	PIR; A32976; IJBNC.	
DR	HSSP; P40189; IBONC.	
DR	InterPro: IPRO01777; .	
DR	InterPro: IPRO03006; .	
DR	Pfam; PF00047; fn3_2.	
DR	Pfam; PF00047; 1g_5.	
KW	Cell adhesion; Glycoprotein; Transmembrane; Repeat;	
KW	Immunoglobulin domain; Alternative splicing; Signal.	
FT	SIGNAL	1..19
FT	CHAIN	20..853
FT		
FT	DOMAIN	20..719
FT	TRANSHEM	720..737
FT	DOMAIN	738..853
FT	DOMAIN	34..103
FT	DOMAIN	132..196
FT	DOMAIN	228..293
FT	DOMAIN	321..401
FT	DOMAIN	428..495
FT	DOMAIN	527..604
FT	DOMAIN	633..700
FT	DOMAIN	152..156
FT	DOMAIN	161..165
FT	DISULFID	41..96
FT	DISULFID	139..189
FT	DISULFID	235..286
FT	DISULFID	328..394
FT	DISULFID	435..488
FT	CARBOHYD	222..222
FT	CARBOHYD	314..314
FT	CARBOHYD	346..346
FT	CARBOHYD	432..432
FT	CARBOHYD	458..458
FT	CARBOHYD	487..487
CC	SEQUENCE	853 AA; 93893 MW; EL2EPQ92JIAVA368 CRC64;

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0Y      63 STUVTVAASNIGDGLTSTF-----BEDIKSDIVQMLKEGVLGHEKREKDE 116
      77 SSSITLIINA-NIDDAGIYKCVYVAEDGTESEAVNKKIKQKLMFKNAPPIPOREBEDA 135
Db
0Y      117 LSEODEM-----FRGTAVPADOV---IVNASLRKLNQVLTDAGTYKCYIITSK 163
      136 YIVCVVSSLEPPIIWKRGDVIILKDKVIREIYLTNNYQLRGICIKKDEGTEYRC-----E 190
Db
0Y      164 G-----KGNANLEYTKGASMP-----YVVDYN-ASSETLCEAPRMFPOPTVWAS 210
      191 GRIIARGLINRKDIOYIVNVPTTYQAROSIYNATANIGOSVTLVCNA-BEGPEPTYSMTK 249
Db
0Y      211 QVDOGANSEVSNSTSEFENSENVTKVYSVLYNVTINNTYSCHIENDIARAAGDI----- 265
      250 DGEQIEN-EDEEKYLFSDSSSELTIRKV----DKNDEAEVYCIENKAGQDASIHUKVF 304
Db
0Y      266 ---KYTESEIKRRSHLOLNNKASLVCSS---FPAISW 297
      305 AKPKITT--YVENQITAMELEOVYLTJCEASGDPIPSITW 340
Db

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Search completed: July 23, 2001, 10:12:20  
Job time: 22 sec

Query Match	8.4%;	Score 132.5;	DB 1;	Length 853;
Best Local Similarity	23.4%;	Pred. No. 0.0043;		
Matches	65;	Conservative	46;	Mismatches 110;
			Indels	57;
			Gaps	14



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OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 22.6 Seconds  
(without alignments)  
1808.949 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574  
Sequence: 1 HASHAHGRQRLHASTQI.....SFFAISMALLPLSPYLMK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :

SPTREMBL.16:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertibrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1425	90.5	282	4 Q9H6B2	Q9H6B2 homo sapien
2	225	14.3	220	4 Q9NM06	Q9NM06 homo sapien
3	225	14.3	414	4 Q9UM44	Q9UM44 homo sapien
4	223	14.2	513	4 Q00481	Q00481 homo sapien
5	223	14.2	513	4 Q9HCY1	Q9HCY1 homo sapien
6	222.5	14.1	347	4 Q9H730	Q9H730 homo sapien
7	220	14.0	280	13 Q73716	Q73716 grus americanus
8	219.5	13.9	286	6 Q46535	Q46535 bos taurus
9	215.5	13.7	731	4 P78409	P78409 homo sapien
10	213.5	13.6	584	4 Q00478	Q00478 homo sapien
11	208.5	13.3	326	4 Q9H458	Q9H458 homo sapien
12	208.5	13.2	334	4 Q9NR44	Q9NR44 homo sapien
13	207.5	13.2	319	4 Q00477	Q00477 homo sapien
14	207.5	13.2	357	4 Q15338	Q15338 homo sapien
15	207.5	13.2	359	4 P78410	P78410 homo sapien
16	207.5	13.2	546	4 Q75658	Q75658 homo sapien
17	204	13.0	350	4 Q99420	Q99420 homo sapien
18	199.5	12.7	290	11 Q9EP73	Q9EP73 mus musculus
19	196	12.5	296	13 Q42404	Q42404 gallus galli

20	195.5	12.4	275	11 Q9JK39	Q9JK39 mus musculus
21	193	12.3	527	4 Q00475	Q00475 homo sapien
22	192	12.2	329	6 Q9XSX6	Q9XSX6 felis silve
23	192	12.2	332	6 Q9GMZ7	Q9GMZ7 felis silve
24	189	12.0	586	4 Q9HCY2	Q9HCY2 homo sapien
25	188.5	12.0	290	4 Q9NZ07	Q9NZ07 homo sapien
26	186	11.8	523	4 P78408	P78408 homo sapien
27	183	11.6	529	4 Q00480	Q00480 homo sapien
28	181	11.5	280	6 Q9TFE1	Q9TFE1 canis famill
29	178	11.3	452	11 Q70355	Q70355 mus musculus
30	176	11.2	313	11 Q35531	Q35531 rattus norv
31	175.5	11.1	455	4 Q9UIR0	Q9UIR0 homo sapien
32	172	10.9	329	6 Q9TFE2	Q9TFE2 canis famill
33	171.5	10.9	272	11 Q70356	Q70356 mus musculus
34	171.5	10.9	432	4 Q9I2C7	Q9I2C7 homo sapien
35	169.5	10.8	284	6 Q9GLJ3	Q9GLJ3 bos taurus
36	168.5	10.7	391	11 Q35441	Q35441 mus musculus
37	166	10.5	326	11 Q70358	Q70358 mus musculus
38	163	10.4	305	7 Q98261	Q98261 homo sapien
39	160.5	10.2	325	6 Q02838	Q02838 sus scrofa
40	153.5	9.8	325	11 Q70359	Q70359 mus musculus
41	152.5	9.7	143	4 Q9NM62	Q9NM62 homo sapien
42	151	9.6	339	13 Q73892	Q73892 gallus galli
43	150.5	9.6	340	13 Q73891	Q73891 gallus galli
44	149.5	9.5	296	6 Q46405	Q46405 bos taurus
45	148	9.4	439	13 Q57349	Q57349 gallus galli

#### ALIGNMENTS

RESULT 1  
ID Q9H6B2 PRELIMINARY: PRT: 282 AA.  
AC Q9H6B2;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE CDNA: FLJ22418 FIS, CLONE HNC08590.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,  
RA Tanaka T., Nakamura Y., Isegaki T., Sugano S.;  
RT "NEO human cDNA sequencing project."  
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK026071; BAB15349.1; -  
SQ SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64;

Query Match	Score	DB 4;	Length	282;
Best local Similarity	99.6%;	Pred. No. 3.5e-110;		
Matches 281;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0;
QY	28	MASLGGILFWSTISIIIIAGATALLTGISGRHSITVTYASAGNIGEDGISTFEP	87	
DB	1	MASLGGILFWSTISIIIIAGATALLTGISGRHSITVTYASAGNIGEDGISTFEP	60	
QY	88	DILSLIVIOWLKEGVIGLVHEFEKSGDELSDEDEFGRRTAVFADQVIVGNASRLKRV	147	
DB	61	DILSLIVIOWLKEGVIGLVHEFEKSGDELSDEDEFGRRTAVFADQVIVGNASRLKRV	120	
QY	148	QLTDACTYCYIITTSKGNANLEYTGAFSMPDEVVDYNASSETLRCAPRFPOPTVY	207	
DB	121	QLTDACTYCYIITTSKGNANLEYTGAFSMPDEVVDYNASSETLRCAPRFPOPTVY	180	
QY	208	WASOVQGANFSEVSTFSELSNENVTMKVSVLVNTINNTYSCMIENDIKATGDIVY	267	
DB	181	WASOVQGANFSEVSTFSELSNENVTMKVSVLVNTINNTYSCMIENDIKATGDIVY	240	

OY 268 TESEIKRSHLOLNSKASLCVSSFFAISWALLPLSPYIMLK 309  
 DB 241 TESEIKRSHLOLNSKASLCVSSFFAISWALLPLSPYIMLK 282

## RESULT 2

O9NM06 PRELIMINARY: PRT: 220 AA.  
 AC O9NM06:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE CDNA FLJ20685 F1S, CLONE KAIJA109.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ILEAL MUCOSA;  
 RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,  
 RA Hiraio M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,  
 RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK000692; BAA91323.1;  
 DR InterPro: IPR003006;  
 DR InterPro: IPR003599;  
 DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00409; Ig: 1.  
 DR SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;  
 SQ

Query Match 14.3%; Score 225; DB 4; Length 220;  
 Best Local Similarity 31.1%; Pred. No. 5.7e-11;

Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

OY 73 GNIGEDGILSCFEPDIKLSIVIQMLKEGYGLVHEFEKGEKDELSEODEMFRGTAVFA 132  
 DB 41 GRLEDDIILPSFE--RGSEVYIMHKYQDSY-KVHSYKSGDHLSDPPRANRTSLFY 96  
 OY 133 DOYVGNASLRKKNQVLDAGYKCIITTSKGGNANLEYKGFASMEPVNDYASSET 192  
 DB 97 NEIQGNASLFFRRVSLDEGIYCYGTAIOVITNKVLYKGVFLTPMKYKRNNTSF 156  
 OY 193 LRCEAPRPFPPVMAVQVDGA---NFSEV-SNTSELSENVTKVSVLYNVT-I 246  
 DB 157 LICSVLSVYPRITW--KMDNTPISENNMERTGSLDPSINSP-----LNTIGS 204  
 OY 247 NNTYSCMIENDIAKAT 262  
 DB 205 NSSYECTIENSLKOT 220

## RESULT 3

O9UM44 PRELIMINARY: PRT: 414 AA.  
 AC O9UM44:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE HERV-H LTR ASSOCIATING PROTEIN 2.  
 GN HHLA2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-99375318; PubMed-10444326;  
 RA Mager D.L., Hunter D.G., Schertzer M., Freeman J.D.;  
 "Endogenous retroviruses provide the primary polyadenylation signal

RT for two new human genes (HHLA2 and HHLA3).".  
 RL Genomics 59:255-263(1999).  
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.

DR EMBL: AF126162; AAD48396.1; -  
 DR InterPro: IPR001039; -  
 DR InterPro: IPR003006; -  
 DR InterPro: IPR003600; -  
 DR Pfam: PF00047; Ig: 2.  
 DR ProDom: PD000050; -; 1.  
 DR SMART: SM00410; IG\_1ike; 1.  
 DR SEQUENCE 414 AA; 46850 MW; D645383E1562F70E CRC64;  
 SQ

Query Match 14.3%; Score 225; DB 4; Length 414;  
 Best Local Similarity 31.1%; Pred. No. 1.4e-10;

Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

OY 73 GNIGEDGILSCFEPDIKLSIVIQMLKEGYGLVHEFEKGEKDELSEODEMFRGTAVFA 132  
 DB 41 GRLEDDIILPSFE--RGSEVYIMHKYQDSY-KVHSYKSGDHLSDPPRANRTSLFY 96  
 OY 133 DOYVGNASLRKKNQVLDAGYKCIITTSKGGNANLEYKGFASMEPVNDYASSET 192  
 DB 97 NEIQGNASLFFRRVSLDEGIYCYGTAIOVITNKVLYKGVFLTPMKYKRNNTSF 156  
 OY 193 LRCEAPRPFPPVMAVQVDGA---NFSEV-SNTSELSENVTKVSVLYNVT-I 246  
 DB 157 LICSVLSVYPRITW--KMDNTPISENNMERTGSLDPSINSP-----LNTIGS 204  
 OY 247 NNTYSCMIENDIAKAT 262  
 DB 205 NSSYECTIENSLKOT 220

## RESULT 4

O00481 PRELIMINARY: PRT: 513 AA.  
 AC O00481:  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE BURYRPHILIN.  
 GN BTF5.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ruddy D.A., Kromal G.S., Lee V.K., Mintier G.A., Quintana L.,  
 RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,  
 RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,  
 RA Wolff R.K., Schatzman R.C., Feder J.N.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: U90552; AAB53430.1; -  
 DR InterPro: IPR000107; -  
 DR InterPro: IPR001870; -  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; Ig: 1.  
 DR Pfam: PF00622; SPRY: 1.  
 DR PRINTS: PR01407; BURYRPHILINCUF.  
 DR SMART: SM00449; SPRY: 1.  
 DR SEQUENCE 513 AA; 57762 MW; CD334D7727CD1F63 CRC64;  
 SQ

Query Match 14.2%; Score 223; DB 4; Length 513;  
 Best Local Similarity 26.4%; Pred. No. 2.7e-10;

Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

OY 62 HSITVTVAASGNI-----GDDGILSCFEPDIKLSIVIQMLKEGYGLVHEFEKGEKDEL 117



QY 82 SCTFEPIKLSIDIVIQMLKEVGLVHEKEKDELSEODEMFRGTAVFADQVYGNAS 141  
 DB 49 PHLSPSPMARSLDIRIMHVOYSEIHYRNEDLDYGDMEEVYGTETLVGRGLSGRDL 108  
 QY 142 LRLKNVOLTDACTYCYITTSKGNANLEYKTGAF-SMPEVNV-D-YNASETLRCEAPR 199  
 DB 109 LRTSGRPDDQGYCTVADGSSYGEATYDLEVSATGSPQLSLEYEGGIRVYCRSAG 168  
 QY 200 WFPQPTVWASQVDOGANESEVSN-T-SFE-----LNSENVTKRVSVLYNVNTIN--TYS 251  
 DB 169 WYPREVLTKD--PGQHLPYSVQSYRSFDERGLFTEVDYI-----VTGDNRCGKMS 218  
 QY 252 CMIEDIAKATGDIKTESEIKRRSLDLNLSKASLCVSS-FF-----AIS 296  
 DB 219 CVYRN-----SHLN-QEOETSLHISAPFHNARPMWGVQVLLVLS 258  
 QY 297 WALLPLSPYL 306  
 DB 259 GVLGLGATL 268

RESULT 8  
 046535 PRELIMINARY: PRT: 286 AA.  
 AC 046535.  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE BUTYROPHILIN (FRAGMENT).  
 GN BTN.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Husaini Y., Wilkins R.J., Davey H.W.;  
 RL Submitted (DCC-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: AF037402; AAB92578.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; Igv; 1.  
 FT NON\_TER 286  
 FT SEQUENCE 286 AA: 32286 MW: 563DA4F372CA353D CXC64;

Query Match 13.9%; Score 219.5; DB 6; Length 286;  
 Best Local Similarity 25.0%; Pred. No. 2.3e-10;  
 Matches 49; Conservative 48; Mismatches 94; Indels 5; Gaps 4;  
 QY 75 IGEGLISCTFEPIKLSIDIVIQMLKEVGLVHEKEKDELSEODEMFRGTAVFADQ 134  
 DB 42 VGEDELPCRLSPNSANGMELRMFRKRYSPAVFVSREGQEGEGEMAEYRGVSLVEDH 101  
 QY 135 VYGNASRLKNVOLTDACTYCYITTSKGNANLEYKTGAF-SMPEVNVYNNASSE-T 192  
 DB 102 IAEGVAVRIQGVKASDGEGRCEFRQDENYEATVHLKVALGSDPHISMKVQESGEIQ 161  
 QY 193 LRCEAPRMFPQPTVWASQVDOGANESEVSN-T-SFELENSENVTKRVSVLYNVNTINNTYSC 252  
 DB 162 LECTSVGVYPERQVOM--RTHRGEEFPMSSESRNDEGLFTVRSVLIIRDSMKNV-SC 218  
 QY 253 MIENDIAKATGDIKVT 268  
 DB 219 CIRNLLGQEKDVEVS 234

RESULT 9  
 P78409

ID P78409 PRELIMINARY: PRT: 731 AA.  
 AC P78409;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE BUTYROPHILIN.  
 GN BT3.3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98044204; PubMed=9382921;  
 RA Tazi-Ahmini R., Henry J., Offer C., Bouissou-Bouchouata C.,  
 RA Mather I.H., Pontarotti P.;  
 RT "Cloning, localization, and structure of new members of the  
 RT butyrophilin gene family in the juxta-telomeric region of the major  
 RT histocompatibility complex.";  
 CC Immunogenetics 47:55-63(1997).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: U97502; AAC02656.1; -.  
 DR EMBL: U97502; AAC02656.1; JOINED.  
 DR EMBL: U97501; AAC02656.1; JOINED.  
 DR EMBL: U90143; AAC02651.1; -.  
 DR InterPro: IPR000107; -.  
 DR InterPro: IPR001870; -.  
 DR InterPro: IPR003006; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00622; SPRY; 1.  
 DR PRINTS: PR01407; BUTYRPHILNCDF.  
 DR SMART: SM00449; SPRY; 1.  
 SQ SEQUENCE 731 AA: 81393 MW: 2F0E0A32B73685F0 CXC64;

Query Match 13.7%; Score 215.5; DB 4; Length 731;  
 Best Local Similarity 25.0%; Pred. No. 1.8e-09;  
 Matches 62; Conservative 49; Mismatches 110; Indels 27; Gaps 9;  
 QY 46 LAGATA-LIIGFISGRHSITVTVASA-----GNIGEDGILSCTFEPIKLS 92  
 DB 1 MASSLAFLNLNPHVS-LFLVQLTTPCSAQFVLAGSPGPIAAVAGDBADPLPCHLFTMSAE 59  
 QY 93 DIVIQMLKEVGLVHEKEKDELSEODEMFRGTAVFADQVYGNASRLKNVOLTDA 152  
 DB 60 TMELKRWSSILQVAVNVADGKEVEYRQSAPIRGRTSILRDSITGAKALRIHNVYASDS 119  
 QY 153 GTYKCYITTSKGNANLEYKTGAFSMPEVNV---YNASETLRCEAPRMFPQPTVWA 209  
 DB 120 GKYLCTYFQHGDPYEKAPVYELKVALG-SDLHTEVAGYDGGIHLCECRSTGWYRQPIWMS 178  
 QY 210 SOVDGANESEVSN-T-SFELENSENVTKRV--SVLYNVNTINNTYSCMIENDI--AKATGDI 265  
 DB 179 D---SKGENIPAVEG---PVNVYGVGLVAVPPVIMTGTSGGVCITINSLIGLEKTASI 233  
 QY 266 KYTESEIK 273  
 DB 234 STADPFIQ 241

RESULT 10  
 000478 PRELIMINARY: PRT: 584 AA.  
 ID 000478.  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE BUTYROPHILIN.  
 GN BT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.



OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ruddy D.A., Kronmal G.S., Lee V.K., Mintier G.A., Quintana L.,  
 RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,  
 RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchinashi Z.,  
 RA Wolff R.K., Schatzman R.C., Feder J.N.;  
 RN Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RL (2)  
 RP SEQUENCE FROM N.A.  
 RA Phillips S.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: U90548; AAB53426.1; -  
 DR EMBL: AL021917; CAI17273.1; -  
 DR InterPro: IPR001070; -  
 DR InterPro: IPR001870; -  
 DR InterPro: IPR003006; -  
 DR Pfam: PF00047; 19; 1.  
 DR Pfam: PF00622; SPRY; 1.  
 DR PRINTS: PR01407; BUTYPHLNCDUF.  
 DR SMART: SM00449; SPRY; 1.  
 SQ SEQUENCE 584 AA; 65001 MW; 2B279B9141E0327F CRC64;

Query Match 13.6%; Score 213.5; DB 4; Length 584;  
 Best Local Similarity 24.6%; Pred. No. 2e-09;  
 Matches 60; Conservative 50; Mismatches 107; Indels 27; Gaps 9;

QY 46 LAALAL-LIIGFISGRHSITVTVA-----GNGEGDILSCTEPDIKLS 92  
 DB 3 MASSLAFLILNFHV--LFLVQLTTPCSAOPSVLPGSPILAMVGEADLPCHFPPTMSAE 61  
 QY 93 DIYIOMLKEGVGLVHEFEKGDLSFODEMFGRTAVFAVOYIVGNASLRKNVQTFDA 152  
 DB 62 TMLRLRWSSSLRQVNVYADGKEVEDRQSAPIYGRITSILDGTTAGAAALRIHNVTRASDS 121  
 QY 153 GTYCYIITSKGNANLEKYGAFSMEPVNV--YNASSETLRCPAPWFPQPIVVA 209  
 DB 122 GKLYCFQDDDFEYKALVELKVALG-SDLHIEVKGEDGIDHLECSGTCWYPOQIKWS 180  
 QY 210 SQYDOGANSEVNTSELSNENYTKV--SYLVNTINNTYSCEIENDI--AKATGDI 265  
 DB 181 D--TKGENIPAV--EAPVADGVGLYAVASVIMRSGSGVSCITIRNSILGLEKTASI 235  
 QY 266 KYTE 269  
 DB 236 SIAD 239

RESULT 11  
 ID 09H458 PRELIMINARY; PRT; 526 AA.  
 AC 09H458;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE BK14H9.2 (BUTYOPHILIN, SUBFAMILY 1, MEMBER A1).  
 GN BTN1A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tracey A.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL121936; CAC16802.1; -  
 SQ SEQUENCE 526 AA; 58960 MW; 4585D5CE88A2ECA4 CRC64;

Query Match 13.3%; Score 209.5; DB 4; Length 526;

Best Local Similarity 26.6%; Pred. No. 3.6e-09;  
 Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;  
 QY 75 IGEDGILSCTFEPPDIKSLDIVIOMLKEGVGLVHEFEKGDLSFODEMFGRTAVFADQ 134  
 DB 42 VGEDADLPCLSLNASEHLELNFRRKVSPLVLRHDSGEAGAEQMPERGRATLVQDS 101  
 QY 135 VIVGNASLRKNVQLDAGTYKCYIITSKGNANLEKYGAF-SMEPVNVYNASSE-T 192  
 DB 102 IAKGRAVALRIRGVRSDDGCTCFREDGSYEALVHLKVALGSDPHISMVOENGEIC 161  
 QY 193 LRCEAPRWFPQPIVVASQYDOGANSEVNTSELSNENYTKVSYLVNTINNTYSC 252  
 DB 162 LECTSVGWPEPQVW--RTSKGEKEPSTSE-SRNPDEBELFTVAASVLIIRTSANVSC 218  
 QY 253 MIEN 256  
 DB 219 YION 222

RESULT 12  
 ID 09NR44 PRELIMINARY; PRT; 334 AA.  
 AC 09NR44;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
 DE BUTYOPHILIN, SUBFAMILY 3, MEMBER A2.  
 GN BTN3A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rhodes D.A., Stammers M., Malcherek G., Beck S., Trowsdale J.;  
 RT "Genomic structure of the btf (butyrophilin-like) gene cluster on  
 human chromosome 6.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF257505; AAF76140.1; -  
 DR InterPro: IPR003006; -  
 DR InterPro: IPR003599; -  
 DR Pfam: PF00047; 19; 1.  
 DR SMART: SM00409; IG; 1.  
 SQ SEQUENCE 334 AA; 36399 MW; 95CPE887DB0DBAE4 CRC64;

Query Match 13.2%; Score 208.5; DB 4; Length 334;  
 Best Local Similarity 26.1%; Pred. No. 2.3e-09;  
 Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGILSCTFEPPDIKSLDIVIOMLKEGVGLVHEFEKGDLSFODEMFGRTAVFADQ 134  
 DB 44 VGEDADLPCLSLNASEHLELNFRRKVSPLVLRHDSGEAGAEQMPERGRATLVQDS 103  
 QY 135 VIVGNASLRKNVQLDAGTYKCYIITSKGNANLEKYGAF-SMEPVNV-DYNASSET 192  
 DB 104 ITGAKALRIHNVYASDSGYLCYFQDGYEKALVELKVALGSDPHISMVOENGEIC 163  
 QY 193 LRCEAPRWFPQPIVW-----ASQYDOGANSEVNTSELSNENYTKVSV 240  
 DB 164 LECRSTGWYPOPIOWGNAGENIPAVEAVVADGVGLYEVA-----ASV 208  
 QY 241 LVNVTINNTYSCEIENDI--AKATGDIKYTE 269  
 DB 209 IMKSGSGEVSCITIRNSILGLEKTASISAD 239

RESULT 13  
 ID 000477 PRELIMINARY; PRT; 319 AA.  
 AC 000477;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)  
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
GN BUTYROPHILIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ruddy D.A., Kromal G.S., Lee V.K., Muttler G.A., Quintana L.,  
Domínguez R., Meyer N.C., Basava A., McClelland E., Fullan A.,  
Maple F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchinashi Z.,  
Wolfe R.K., Schatzman R.C., Feder J.N.;  
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: U90546; AAB53424.1; -  
DR InterPro: IPR003006; -  
DR SMART: PF00047; 19; 1.  
DR SMART: SM00409; 19; 1.  
SQ SEQUENCE 319 AA; 34734 MW; 1697EF524F558749 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 319;  
Best Local Similarity 26.1%; Pred. No. 2.7e-09;  
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSDIVIQMLKEGVLGVHEFKEGKDELSPQDEMRGRITAVFAQ 134  
DB 44 VEDDADLPCHLPPTMSAETMELKWSLSRQVYVYADKEVEDQSAFYRGRTSILRDG 103  
QY 135 VIVGNASLRKLVNLTDACTYCYITTSKGNANLEYKTGA-F-SMPEYV-N-DYNASSET 192  
DB 104 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYKEDGGIH 163  
QY 193 LKCEAPRPFPPPTVW-ASQVDQGANSEVSNTSELSNENVTMKVSV 240  
DB 164 LECRSTGWYPOQIOWSNAGENIPAVEAPVYADVGLGEYVA-ASV 208  
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269  
DB 209 IMRGSSEGVSCITRNSLGLKTAISTAD 239  
RESULT 14  
ID 015338 PRELIMINARY; PRT: 357 AA.  
AC 015338;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE BUTYROPHILIN.  
GN BT3.2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98044204; PubMed=9382921;  
Tazi-Ahni R., Henry J., Offer C., Bouissou-Bouchouata C.,  
Mather I.H., Pontarotti P.;  
"Cloning, localization, and structure of new members of the  
butyrophilin gene family in the juxta-telomeric region of the major  
histocompatibility complex";  
Immunogenetics 47:55-63(1997).  
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: U97498; AAC02655.1; -  
DR EMBL: U97498; AAC02655.1; JOINED.  
DR InterPro: IPR003006; -

DR InterPro: IPR003599; -  
DR Pfam: PF00047; 19; 1.  
DR SMART: SM00409; 19; 1.  
SQ SEQUENCE 357 AA; 39245 MW; A6BECA1D6B2C105 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 357;  
Best Local Similarity 26.1%; Pred. No. 3.1e-09;  
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSDIVIQMLKEGVLGVHEFKEGKDELSPQDEMRGRITAVFAQ 134  
DB 42 VEDDADLPCHLPPTMSAETMELKWSLSRQVYVYADKEVEDQSAFYRGRTSILRDG 101  
QY 135 VIVGNASLRKLVNLTDACTYCYITTSKGNANLEYKTGA-F-SMPEYV-N-DYNASSET 192  
DB 102 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYKEDGGIH 161  
QY 193 LKCEAPRPFPPPTVW-ASQVDQGANSEVSNTSELSNENVTMKVSV 240  
DB 162 LECRSTGWYPOQIOWSNAGENIPAVEAPVYADVGLGEYVA-ASV 206  
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269  
DB 207 IMRGSSEGVSCITRNSLGLKTAISTAD 237

RESULT 15  
ID P78410 PRELIMINARY; PRT: 359 AA.  
AC P78410;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE BUTYROPHILIN PROTEIN.  
GN BT3.2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98044204; PubMed=9382921;  
Tazi-Ahni R., Henry J., Offer C., Bouissou-Bouchouata C.,  
Mather I.H., Pontarotti P.;  
"Cloning, localization, and structure of new members of the  
butyrophilin gene family in the juxta-telomeric region of the major  
histocompatibility complex";  
Immunogenetics 47:55-63(1997).  
RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: U90144; AAC02652.1; -  
DR InterPro: IPR003006; -  
DR InterPro: IPR003599; -  
DR Pfam: PF00047; 19; 1.  
DR SMART: SM00409; 19; 1.  
SQ SEQUENCE 359 AA; 39444 MW; 3CB2DA61322593B8 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 359;  
Best Local Similarity 26.1%; Pred. No. 3.1e-09;  
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSDIVIQMLKEGVLGVHEFKEGKDELSPQDEMRGRITAVFAQ 134  
DB 44 VEDDADLPCHLPPTMSAETMELKWSLSRQVYVYADKEVEDQSAFYRGRTSILRDG 103  
QY 135 VIVGNASLRKLVNLTDACTYCYITTSKGNANLEYKTGA-F-SMPEYV-N-DYNASSET 192  
DB 104 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYKEDGGIH 163  
QY 193 LKCEAPRPFPPPTVW-ASQVDQGANSEVSNTSELSNENVTMKVSV 240  
DB 162 LECRSTGWYPOQIOWSNAGENIPAVEAPVYADVGLGEYVA-ASV 206  
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269  
DB 207 IMRGSSEGVSCITRNSLGLKTAISTAD 237

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Page 7

Db 164 LECRSTGWYPPQIOIOMNAKENIPAVEAPVADGVGLYEVA-----ASV 208

OY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269

Db 209 IMRGSGEVSCIIIRNSLGLKXTASISIA 239

Search completed: July 23, 2001, 10:13:30  
Job time: 92 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 20.63 Seconds

(without alignments)  
908.037 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574  
Sequence: 1 HASAHASRQROHLSASTQT.....SSFRAISWALLPLSPYLMK 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_0601.\*  
1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
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14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
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17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	21	AA12556
2	1431	90.9	282	21	AA12557
3	1431	90.9	282	21	AA12557
4	1431	90.9	282	21	AA12557
5	1431	90.9	282	21	AA12557
6	842.5	53.5	195	22	AA65242
7	246	15.6	387	22	AA65242
8	246	15.6	387	22	AA65242
9	246	15.6	387	22	AA65242
10	241	15.3	316	20	AA41705
11	241	15.3	316	21	AA44261

12	239	15.2	316	22	AA87394	Human gene 2 encod
13	239	15.2	534	22	AA87249	Human amyloid prec
14	232.5	14.8	516	22	AA87417	Human gene 2 encod
15	225.5	14.3	466	21	AA99413	Human PRO1472 (UNQ
16	225.5	14.3	466	22	AA87577	Human PRO1472. Ho
17	225.5	14.3	466	22	AA86162	Protein of the Inv
18	225	14.3	327	22	AA80415	Gene #1 associated
19	225	14.3	349	22	AA80414	Gene #1 associated
20	225	14.3	414	22	AA80371	Secreted protein e
21	224.5	14.3	461	21	AA85591	Protein encoded by
22	223	14.2	513	19	AA878918	Bovine butyrophill
23	222.5	14.1	461	21	AA85615	Human secreted pro
24	222.5	14.1	500	21	AA99385	Human PRO1347 (UNQ
25	222.5	14.1	500	22	AA87567	Human PRO1347. Ho
26	222.5	14.1	500	22	AA86134	Protein of the Inv
27	219.5	13.9	193	22	AA860775	Gene 47 related pe
28	219.5	13.9	526	20	AA897812	Bovine butyrophill
29	218	13.9	319	21	AA85584	BHR II protein en
30	213.5	13.6	584	19	AA878916	Bovine butyrophill
31	211.5	13.4	526	20	AA897814	Human butyrophill
32	209	13.3	223	19	AA871593	Human myelin oligo
33	207.5	13.2	319	19	AA878917	Bovine butyrophill
34	207.5	13.2	331	19	AA871592	Human myelin oligo
35	207.5	13.2	334	20	AA89661	Human secreted pro
36	202	12.8	524	20	AA897815	Human secreted pro
37	199.5	12.7	250	22	AA872646	Guinea pig butyrop
38	193	12.3	527	19	AA878914	Murine B7-4 protei
39	192	12.2	329	21	AA83285	Feline CD86 (B7-2)
40	192	12.2	329	21	AA83285	Feline CD86 (B7-2)
41	192	12.2	332	20	AA41079	Cat CD86 (B7-2) 11
42	188.5	12.0	290	22	AA872645	Feline B7-2 protei
43	183	11.6	523	19	AA878915	Human B7-4 membran
44	182	11.6	245	22	AA872644	Bovine butyrophill
45	181	11.5	280	20	AA841078	Human B7-4 secreta

## ALIGNMENTS

RESULT	1
AA12556	AA12556 standard; Protein; 309 AA.
ID	AA12556;
AC	AA12556;
XX	07-NOV-2000 (first entry)
DE	Human ovarian carcinoma antigen OBE protein SEQ ID NO:392.
XX	Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW	tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX	
OS	Homo sapiens.
XX	
PN	W0200036107-A2.
XX	
PD	22-JUN-2000.
XX	
PF	17-DEC-1999; 99WO-0530270.
XX	
PR	17-DEC-1998; 98US-0215681.
PR	17-DEC-1998; 98US-0216003.
PR	23-JUN-1999; 99US-0338933.
PR	24-SEP-1999; 99US-0404879.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Mitcham JL, King GE, Algate PA, Frudakis TN;
DR	WPI; 2000-431589/37.
XX	
PT	Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of

PT cancer, preferably ovarian cancer -

XX  
XX  
PS Example 2; Page 205-206; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytosolic activity and can be used in gene therapy and vaccines.  
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines  
CC are useful for the prevention, diagnosis and treatment of cancer,  
CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557  
CC represent human ovarian carcinoma polynucleotides and proteins used in  
CC the exemplification of the present invention.

XX  
XX  
SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 21; Length 309;  
Best Local Similarity 100.0%; Pred. No. 1.9e-131;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGROROLHSASTOIRWEPSPAMASLGQILFWSIISIIIIAGALIIIGFGISG 60  
DB 1 hasahasgrqrlhasastqirwepspamaslqgllfwsllsllllagalaillgfglsq 60  
QY 61 RHSTIVTVASAGNIGEDGILSCTFEPIKLSDIVIQWLKEGVGLVHEFKEGKDELSEQ 120  
DB 61 rhtstvtvasagnlgedgllsctfepdklsdviyqlwkegvglvhefkegkdelseq 120  
QY 121 DEMFGRTAVFADQYIVGNASLRKLNQUTDAGTYCYITTSKGNANLEKTKGAFSMP 180  
DB 121 demfgrtafvadqyivgnaslrlnknvqldagtykcylltskkganllekktgafsm 180  
QY 181 EYVNDYNASSETLRCEAPRPFQPTVVASQVDOGANFSEVNTSEFELSENVTMKVSV 240  
DB 181 evnvdynassetlrceaprfpqptvvasqvdoganfsevnstefelsenvtmkvsv 240  
QY 241 LYNNNTNNYSCMIENDIAKATGDIKVTSEIKRSHLQOLNSKASLCVSSFFAISWALL 300  
DB 241 lynnntnnyscmiendiakatgdiikvtseikrshlqolnskaslcvsffaiswall 300  
QY 301 PLSPYLMLK 309  
DB 301 plspylmlk 309

RESULT 2  
AAB12557  
ID AAB12557 standard; Protein: 282 AA.

XX  
XX  
AC AAB12557;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE Human ovarian carcinoma antigen O8E protein SEQ ID NO:393.  
XX  
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;  
XX tumour antigen; identification; cytostatic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200036107-A2.  
XX  
PD 22-JUN-2000.  
XX  
PE 17-DEC-1999; 99WO-US30270.  
XX  
PF 17-DEC-1998; 98US-0215681.  
XX  
PR 17-DEC-1998; 98US-0216003.  
XX  
PR 23-JUN-1999; 99US-0338933.  
XX  
PR 24-SEP-1999; 99US-0404879.  
XX  
PA (CORI-) CORIXA CORP.

XX  
PI Mitcham JL, King GE, Algate PA, Frudakis TN;  
XX  
XX WPI; 2000-431589/37.  
XX  
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic  
CC acid encoding it, useful for the diagnosis, prevention and treatment of  
PT cancer, preferably ovarian cancer -

XX  
XX  
PS Example 2; Page 207; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an  
CC immunogenic portion of an ovarian carcinoma protein (or its variants).  
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have  
CC cytosolic activity and can be used in gene therapy and vaccines.  
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines  
CC are useful for the prevention, diagnosis and treatment of cancer,  
CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557  
CC represent human ovarian carcinoma polynucleotides and proteins used in  
CC the exemplification of the present invention.

XX  
XX  
SQ Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 21; Length 282;  
Best Local Similarity 100.0%; Pred. No. 7.3e-119;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIISIIIIAGALIIIGFGISGRHSITVTVASAGNIGEDGILSCTFEP 87  
DB 1 maslqgllfwsllsllllagalaillgfglsgrhsitvtvasagnlgedgllsctfep 60  
QY 88 DIKLSDIVIQWLKEGVGLVHEFKEGKDELSEQDEMFRGRTAVFADQYIVGNASLRKNV 147  
DB 88 dklksdviyqlwkegvglvhefkegkdelseqdemfgrtafvadqyivgnaslrlnv 120  
QY 148 QLTDAQTYCYITTSKGNANLEKTKGAFSMP EYVNDYNASSETLRCEAPRPFQPTV 207  
DB 148 qldagtykcylltskkganllekktgafsmpevndynassetlrceaprfpqptcv 180  
QY 208 WASOVDGANFSEVNTSEFELSENVTMKVSVLYNNNTNNYSCMIENDIAKATGDIKV 267  
DB 208 wasovdganfsevnstefelsenvtmkvsvlynnntnnyscmiendiakatgdi 240  
QY 268 TESEIKRSHLQOLNSKASLCVSSFFAISWALLPLSPYLMLK 309  
DB 241 teseikrshlqolnskaslcvsffaiswallplspylmlk 282

RESULT 3  
AAV66719  
ID AAV66719 standard; Protein: 282 AA.

XX  
XX  
AC AAV66719;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1291.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO9963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PE 02-JUN-1999; 99WO-US12252.  
XX  
PF 02-JUN-1998; 98US-0087607.  
XX  
PR 02-JUN-1998; 98US-0087609.  
XX  
PR 02-JUN-1998; 98US-0087735.  
XX  
PA

PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
PR 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
PR 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
PR 04-JUN-1998; 98US-0088036.  
PR 05-JUN-1998; 98US-0088167.  
PR 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
PR 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089603.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090676.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090680.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.

PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091638.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092470.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.  
PR 04-AUG-1998; 98US-0095285.  
PR 04-AUG-1998; 98US-0095301.  
PR 04-AUG-1998; 98US-0095302.  
PR 04-AUG-1998; 98US-0095318.  
PR 04-AUG-1998; 98US-0095321.  
PR 04-AUG-1998; 98US-0095325.  
PR 10-AUG-1998; 98US-0095916.  
PR 10-AUG-1998; 98US-0095929.  
PR 10-AUG-1998; 98US-0096012.  
PR 11-AUG-1998; 98US-0096143.  
PR 11-AUG-1998; 98US-0096146.  
PR 12-AUG-1998; 98US-0096329.  
PR 17-AUG-1998; 98US-0096757.  
PR 17-AUG-1998; 98US-0096766.  
PR 17-AUG-1998; 98US-0096768.  
PR 17-AUG-1998; 98US-0096773.  
PR 17-AUG-1998; 98US-0096791.  
PR 17-AUG-1998; 98US-0096867.  
PR 17-AUG-1998; 98US-0096891.  
PR 17-AUG-1998; 98US-0096894.  
PR 17-AUG-1998; 98US-0096895.  
PR 17-AUG-1998; 98US-0096897.  
PR 18-AUG-1998; 98US-0096949.  
PR 18-AUG-1998; 98US-0096950.  
PR 18-AUG-1998; 98US-0096959.  
PR 18-AUG-1998; 98US-0096960.  
PR 18-AUG-1998; 98US-0097022.  
PR 19-AUG-1998; 98US-0097141.  
PR 20-AUG-1998; 98US-0097218.  
PR 24-AUG-1998; 98US-0097661.  
PR 26-AUG-1998; 98US-0097951.  
PR 26-AUG-1998; 98US-0097952.  
PR 26-AUG-1998; 98US-0097954.  
PR 26-AUG-1998; 98US-0097955.  
PR 26-AUG-1998; 98US-0097971.  
PR 26-AUG-1998; 98US-0097974.  
PR 26-AUG-1998; 98US-0097978.  
PR 26-AUG-1998; 98US-0097979.  
PR 26-AUG-1998; 98US-0097986.  
PR 26-AUG-1998; 98US-0098014.  
PR 31-AUG-1998; 98US-0098325.  
PR 16-SEP-1998; 98US-0100634.  
PR 12-JAN-1999; 99US-0115565.  
  
XX PA (GETH ) GENENTECH INC.  
XX PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
XX PI Wood WI, Yuan J;  
XX XX  
DR WPI, 2000-072883/06.  
XX N-PSDB; AAZ65059.  
XX DR  
XX PT  
XX PS  
XX  
Membrane-bound proteins and related nucleotide sequences -  
claim 12, Fig 208; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIR  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO molecule inhibitors  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
CC will also be useful for the preparation of PRO polypeptides, especially  
CC by recombinant techniques.

SO Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 21; Length 282;  
Best Local Similarity 100.0%; Pred. No. 7.5e-119;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFWSTIIITIIAGAILGIGISGRHSITVTYVASAGNIGEDGILSCTFEP 87  
DB 1 maslqgilfwstllstlllagaalallgfglsgrhsiltvtvasagnigedgillsctfep 60  
QY 88 DIKLSDIVIOWLKEVGLVHFEKSGKDELSEODEMFRGRTAVFADQVIVGNASRLKRV 147  
DB 61 dklldslvliwqlkevgllvghfekegkdelseodemfrgtrtavfadvivgnasrlrkvv 120  
QY 148 QLTDACTYCYIITTSKGKGNANLEKYGAFSMEPVNDYNASSETLRCAPRWFPQPTVY 207  
DB 121 qltdagtykcyiitstskggnanleyktgafsmpevndvynassetlrceaprwfpqptvv 180  
QY 208 WASOVDOGANFSEVSWTSELSSENENTMKVSVLYVNTNNTNSCMIEENDIKAKGDIKV 267  
DB 181 wasqvodganfsevsntsfelnsenentmkvsvlyvntnntnyscmiendikakagdklv 240  
QY 268 TSEIKRRSHLQILNSKASLCVSSFFPAISWALLPLSPYLMLK 309  
DB 241 tseikrrshlqlnksaslcvssffaiswallplspylmlk 282

RESULT 4  
AAB87555  
ID AAB87555 standard; Protein; 282 AA.  
XX  
AC AAB87555;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Human PRO1291.  
XX  
KW Human; PRO protein; mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO200116318-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 24-AUG-2000; 2000WO-US23328.  
XX  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
XX

PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 05-JUN-2000; 2000US-0209832.

PA (GETH ) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

DR WPI: 2001-183260/18.  
DR N-PSDB: AAF92087.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping.

PS Claim 12; Fig 60; 278bp; English.

CC The present sequence is a human PRO polypeptide (secreted and  
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
CC anti-PRO antibodies are useful for preparation of a medicament useful in  
CC the treatment of a condition which is responsive to the PRO protein,  
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping.

SO Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 22; Length 282;  
Best Local Similarity 100.0%; Pred. No. 7.5e-119;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFWSTIIITIIAGAILGIGISGRHSITVTYVASAGNIGEDGILSCTFEP 87  
DB 1 maslqgilfwstllstlllagaalallgfglsgrhsiltvtvasagnigedgillsctfep 60  
QY 88 DIKLSDIVIOWLKEVGLVHFEKSGKDELSEODEMFRGRTAVFADQVIVGNASRLKRV 147  
DB 61 dklldslvliwqlkevgllvghfekegkdelseodemfrgtrtavfadvivgnasrlrkvv 120  
QY 148 QLTDACTYCYIITTSKGKGNANLEKYGAFSMEPVNDYNASSETLRCAPRWFPQPTVY 207  
DB 121 qltdagtykcyiitstskggnanleyktgafsmpevndvynassetlrceaprwfpqptvv 180  
QY 208 WASOVDOGANFSEVSWTSELSSENENTMKVSVLYVNTNNTNSCMIEENDIKAKGDIKV 267  
DB 181 wasqvodganfsevsntsfelnsenentmkvsvlyvntnntnyscmiendikakagdklv 240  
QY 268 TSEIKRRSHLQILNSKASLCVSSFFPAISWALLPLSPYLMLK 309  
DB 241 tseikrrshlqlnksaslcvssffaiswallplspylmlk 282

RESULT 5  
AAB65242  
ID AAB65242 standard; Protein; 282 AA.  
XX  
AC AAB65242;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1291 (UNQ659) protein sequence SEQ ID NO:291.  
XX  
KW Human; secreted and transmembrane protein; PRO: cytosolic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX



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PD 07-DEC-2000.
XX
XX 30-MAR-2000: 2000MO-US08439.
PF
PR 02-JUN-1999: 99MO-US12252.
XX 23-JUN-1999: 99US-0141037.
PR 07-JUL-1999: 99US-0143048.
XX 20-JUL-1999: 99US-0144758.
PR 26-JUL-1999: 99US-0145698.
XX 28-JUL-1999: 99US-0146222.
PR 17-AUG-1999: 99US-0149396.
XX 15-SEP-1999: 99MO-US21090.
PR 15-SEP-1999: 99MO-US21547.
XX 08-OCT-1999: 99US-0158663.
PR 30-NOV-1999: 99MO-US28313.
XX 01-DEC-1999: 99MO-US28301.
PR 16-DEC-1999: 99MO-US30095.
XX 20-DEC-1999: 99MO-US30911.
PR 05-JAN-2000: 2000MO-US00219.
XX 06-JAN-2000: 2000MO-US00376.
PR 11-FEB-2000: 2000MO-US03565.
XX 18-FEB-2000: 2000MO-US04341.
PR 22-FEB-2000: 2000MO-US04414.
XX 24-FEB-2000: 2000MO-US04914.
PR 24-FEB-2000: 2000MO-US05004.
XX 02-MAR-2000: 2000MO-US05841.
PR 15-MAR-2000: 2000MO-US06884.
XX 20-MAR-2000: 2000MO-US07377.
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnuyers L, Eaton DL,
PI Ferrara N, Fong S, Geider H, Gerltsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurey AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX MPI: 2001-032160/04.
DR N-PSDB; AAF44205.
XX
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 208; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX Sequence 282 AA:
SQ

```

```

Query Match          90.9%; Score 1431; DB 22; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.5e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 28 MASLGQILFMSIISIIILAGAILIGFISGRHSITVTVAAGNIGEDGILSCFEP 87
   |||||||
DB 1 maslqgilfmsiisiiilagaiallfgfsgsrhsitvtvasagnlgedgilsctfep 60
OY 88 DIKLSIDIVOMLKEGVGLVHEFEKDELSDEDMFRGRTAVFADQIVYGNASLRKLV 147
   |||||||

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DB 61 diktstdiviqwkegyilvhefkegkdelseqdemtrgrtavladyivgnaslrkvn 120
   |||||||
OY 148 QLTDACTYKCYIITTSKGNANLEKRTGAFSMEPVNDVYNASSETLRCEAPRPFPOPTV 207
   |||||||
DB 121 qltdagtykcyiitlskgnanlekyktgafsmpevndvynassectlrceaprvfpqptlv 180
OY 208 WASOVQGANFSEVSNFSFELNSENVMKVSVLYXNTTNTSCMTENDIAKATGDIKV 267
   |||||||
DB 181 wasqvqganfsevsntsfelnsevmkvsvlyxnttntscmtendlakatkqikv 240
OY 268 TSESIKRRSHQLNLSKASCLVCSFPAISWALLPLSPYLMLK 309
   |||||||
DB 241 teseikrrshqlnlskascvcsfpaiswallplspylmlk 282

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RESULT 6
AAB60776
ID AAB60776 standard; peptide; 195 AA.
XX
XX AAB60776;
AC
XX 27-MAR-2001 (first entry)
DT
XX
XX Gene 47 related peptide #2.
DE
XX
XX Secreted protein; gene therapy; vaccine; cancer; leukemia;
KW autoimmune disease; allergy; inflammation; graft rejection;
KW hyperproliferation; cardiovascular; infection.
XX
XX Homo sapiens.
OS
XX
XX WO200076531-A1.
PN
XX 21-DEC-2000.
PD
XX
XX 01-JUN-2000: 2000MO-US15137.
PF
XX
XX 11-JUN-1999: 99US-0138625.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
PI
XX
XX MPI: 2001-071148/08.
DR
XX
XX Nucleic acids encoding 47 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX
XX Disclosure; Page 524-525; 525pp; English.
XX
XX The present invention relates to 26 secreted human proteins. The
CC proteins may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate polypeptide expression.
CC For example, they may be used in gene therapy or in vaccines.
CC Typical of diseases which are potentially treatable are cancers
CC (including leukemia), autoimmune diseases, allergies, inflammation,
CC graft rejection, hyperproliferation, cardiovascular diseases
CC (particularly critical limb ischemia and coronary disease) and any
CC involving abnormal angiogenesis, neurodegeneration and/or
CC infectious diseases.
XX
XX Sequence 195 AA:
SQ

```

```

Query Match          53.5%; Score 842.5; DB 22; Length 195;
Best Local Similarity 82.1%; Pred. No. 5.8e-67;
Matches 170; Conservative 3; Mismatches 9; Indels 25; Gaps 2;

```

```

OY 75 IGEDEGILSCFPEPDIKLSIDIVOMLKEGVGLVHEFEKDELSDEDMFRGRTAVFAD- 133
   |||||||
DB 1 lgeegilscfpepdklisddivomlkegyilvhefkegq-----lxaavgax 48

```

QY 134 -----QVIVGNASLRKLVOLTDAGTYKCYITTSKSGKNANLEYKGAFSMPE 181  
 Db 49 nvrp9gqcllkkxllampllrlknvgiltadgtykcylltsykgknanleytgaftsmpe 108  
 QY 182 VAVDYNASSETLRCEAPRWFPOPTVWVASQVDOGANFSEVNTSELSNENTMKVSVL 241  
 Db 109 vnvdyNASSETLRCEAPRWFPGPTLVWASQVDOGANFSEVNTSELSNENTMKVSVL 168  
 QY 242 VAVTINNTYSCMIENDIAKATGDIKVT 268  
 Db 169 ynvltinntyscmIendiaKATgdiKvt 195  
 RESULT 7  
 AAB87415  
 ID AAB87415 standard; Protein; 387 AA.  
 AC AAB87415;  
 XX  
 DT 22-MAY-2001 (first entry)  
 DE Human gene 2 encoded secreted protein fragment, SEQ ID NO:156.  
 XX  
 KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angioygenic disorder; kidney disorder;  
 KW gastrointestlnal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnerary;  
 KW cell culture; chemotaxis; food additive;  
 KW binding partner identification.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200118022-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000WO-US24008.  
 XX  
 PR 03-SEP-1999; 99US-0152315.  
 PR 03-SEP-1999; 99US-0152317.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI NI J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;  
 PI Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;  
 PI Moore PA, Shi Y, Wei Y, Florence KA;  
 XX  
 DR WPI: 2001-203081/20.  
 XX  
 PT Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -  
 XX  
 PS Disclosure: Page 14; 607pp; English.  
 XX  
 CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted  
 CC protein genes, and AAB87342-AAB87413 represent the proteins they encode.  
 CC AAB87414-AAB87454 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 52 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,

CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angioygenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention.  
 CC  
 SQ Sequence 387 AA;  
 XX  
 Query Match 15 6%; Score 246; DB 22; Length 387;  
 Best Local Similarity 26.2%; Pred. No. 9,7e-14;  
 Matches 76; Conservative 55; Mismatches 11; Indels 48; Gaps 13;  
 QY 19 QIRWEPSPMAALGOT-----LF--WSIIISIIILAGAILIGFGI---SGRHS 63  
 Db 28 efwqdgqgvphtgnvtsqmanegqlfwhvhlrvvgangtyesclvnpvrlqgdahs 87  
 QY 64 IVTVTVAS-----AGNIGEDGILSCFP--EPDIKLSDIVIWLKEGYLGLV 107  
 Db 88 viltqprspfgavvevqdpvvalvgtdatlhcsfpepgfsltqlnllwqldtckqv 147  
 QY 108 HEPKECKDELSPODEMFERRTAVFPADQVVGNASRLKKNVOLTDGTYKCYITTSKGN 167  
 Db 148 hsftegrd---qgsayanrtalfpollagnasrlqvravadgstfct-vslrdgys 202  
 QY 168 ANLEKKTGA-FSMPEVNVVDY-----ASSETLRCEAPRWFPOPTVWVASQVDOGANFSEV 221  
 Db 203 aavslqvaaprykpmntlepnkdlrpgdvtlltcsayrygpeaefw--qdgqgypplgn 260  
 QY 222 SNTSELSNENTMKVSVLVNVT--INNTYSCMIENDIAK--ATGDIKVT 268  
 Db 261 vltvts-qmanegllfdvhsylrvlvgangtyesclvnpvrlqgdahsvlt 309  
 RESULT 8  
 AAB88459  
 ID AAB88459 standard; Protein; 534 AA.  
 AC AAB88459;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human membrane or secretory protein clone PSEC0249.  
 KW Human; secretory protein; membrane protein; vaccine; gene therapy;  
 KW rheumatoid arthritis; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1067182-A2.  
 XX  
 PD 10-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114090.  
 XX  
 PR 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX

PI Oka T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
XX WPI: 2001-093989/11.  
DR N-PSDB: AAF93886.  
XX  
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in  
XX gene therapy or as candidate target molecules in drug development -  
PS Claim 1: SEQ ID 286; 609pp + CD ROM; English.  
XX  
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916  
CC which encode human secretory or membrane proteins represented by  
CC AAF88317 - AAF88419. Included in the invention are primers  
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the  
CC cDNA sequences of the invention. The invention also includes methods for  
CC the production of antibodies directed against the proteins, and cDNA  
CC sequences, which can be used in vaccines. The polynucleotide sequences  
CC can be used in gene therapy. The polynucleotide sequences and the  
CC proteins they encode may be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate secretory  
CC protein/membrane protein expression. The nucleic acids and complementary  
CC sequences may also be used as DNA probes in diagnostic assays  
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
CC presence of similar nucleic acid sequences in samples. They may also be  
CC used to study the expression and function of secretory proteins/membrane  
CC polypeptides and their role in metabolism. The polypeptides may be used  
CC as antigens in the production of antibodies against them and in assays to  
CC identify modulators (agonists and antagonists) of expression and  
CC activity. The antibodies and antagonists may also be used as therapeutic  
CC agents to down regulate expression and activity. The antibodies may also  
CC be used as diagnostic agents for detecting the presence of the  
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
CC (ELISA)). Examples of diseases which may be treated include Rheumatoid  
CC arthritis and diabetes.  
XX  
SQ Sequence 534 AA;

Query Match 15.6%; Score 246; DB 22; Length 534;  
Best Local Similarity 26.2%; Pred. No. 1.5e-13;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

YY 19 QIRPEPSPAMASLQI-----LF--WSIISIIIIAGALALIGFIC---SGRHS 63  
DB 175 evfmgdggvplgtvntsgmaneglfidvnsilrvlgangtysclvrnpvlqgdahs 234  
YY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIRKSDIVIQMLKGVGLV 107  
DB 235 vtlfpqspitgavveqvpedpvalvgtldatlrscfspepgfsiaqlnlwqltdtkqlv 294  
YY 108 HEFKEGDELSEODEMFRGRTAVFADOVIVGNASLRKNVQLTDAGTYKCYIIRSKGKN 167  
DB 295 hsftegrd-----ggsayantalfpdlaggnaslrigrvradegsfctf-vslrdfigs 349  
YY 168 ANLEYKTGA-FSMEVNVN-----ASSETLRCEADRMFPQPTVWASOVDOGANSEV 221  
DB 350 aavslgvaapysksmlepkdlrpgdvtlftcsyrygpeaevf--qdgqgvpltn 407  
YY 222 SNTSEFLENSEVTKVSVLYNVT-INNTYSCEMIENDIAK--ATGDIKVT 268  
DB 408 vltsgmaneglfidvnsilrvlgangtysclvrnpvlqgdahsvltit 456

RESULT 9  
ID AAB27250 standard; Protein; 534 AA.  
XX  
AC AAB27250;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Human amyloid precursor protein protease SEQ ID NO: 4.  
XX

KW Human; amyloid precursor protein protease; Alzheimer's disease;  
KM neurodegenerative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200068266-A1.  
XX  
PD 16-NOV-2000.  
XX  
PF 09-MAY-2000; 2000WO-US06707.  
XX  
PR 11-MAY-1999; 99US-0133423.  
XX  
PA (EIL) LILLY & CO ELI.  
XX  
PI Becker GW, Hale JE, Heath WF, Johnstone EM, Little SP, Tu Y;  
PI Yeh W, Yin T;  
XX  
DR WPI: 2001-016080/02.  
DR N-PSDB: AAC66922.  
XX  
PT New amyloid precursor protein proteases and nucleic acids useful for  
PT identifying amyloid precursor protein protease inhibitors for treating  
PT or preventing Alzheimer's disease and other neurodegenerative diseases  
XX  
PS Claim 1; Page 7-9; 82pp; English.  
XX  
XX The present sequence is a human amyloid precursor protease protein.  
CC Amyloid precursor protein builds up in the brain of individuals with  
CC Alzheimer's disease, and the sequences of the invention can be used to  
CC identify compounds which can be used to prevent and treat the disease. In  
CC addition, they are suitable for use in the treatment of other  
CC neurodegenerative diseases, Down's syndrome and hereditary cerebral  
CC haemorrhage with amyloidosis of the Dutch-type (HCHWA-D).  
XX  
SQ Sequence 534 AA;

Query Match 15.6%; Score 246; DB 22; Length 534;  
Best Local Similarity 26.2%; Pred. No. 1.5e-13;  
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

YY 19 QIRPEPSPAMASLQI-----LF--WSIISIIIIAGALALIGFIC---SGRHS 63  
DB 175 evfmgdggvplgtvntsgmaneglfidvnsilrvlgangtysclvrnpvlqgdahs 234  
YY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIRKSDIVIQMLKGVGLV 107  
DB 235 vtlfpqspitgavveqvpedpvalvgtldatlrscfspepgfsiaqlnlwqltdtkqlv 294  
YY 108 HEFKEGDELSEODEMFRGRTAVFADOVIVGNASLRKNVQLTDAGTYKCYIIRSKGKN 167  
DB 295 hsftegrd-----ggsayantalfpdlaggnaslrigrvradegsfctf-vslrdfigs 349  
YY 168 ANLEYKTGA-FSMEVNVN-----ASSETLRCEADRMFPQPTVWASOVDOGANSEV 221  
DB 350 aavslgvaapysksmlepkdlrpgdvtlftcsyrygpeaevf--qdgqgvpltn 407  
YY 222 SNTSEFLENSEVTKVSVLYNVT-INNTYSCEMIENDIAK--ATGDIKVT 268  
DB 408 vltsgmaneglfidvnsilrvlgangtysclvrnpvlqgdahsvltit 456

RESULT 10  
ID AAY41705 standard; Protein; 316 AA.  
XX  
AC AAY41705;  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO352 protein sequence.  
XX





DR N-PSDB: AAF91910.  
XX Nucleic acid molecules encoding human secreted proteins, used in  
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
PT Parkinson's diseases and cancers -  
XX  
PS Claim 11; Page 563-564; 607pp; English.  
XX  
CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted  
CC protein genes, and AAB87344-AAB87413 represent the proteins they encode.  
CC AAB87414-AAB87454 represent human secreted protein fragments. The genes  
CC and their corresponding secreted proteins are useful for preventing,  
CC treating or ameliorating medical conditions, e.g., by protein or gene  
CC therapy. Pathological conditions can be diagnosed by determining the  
CC amount of the new protein in a sample or by determining the presence of  
CC mutations in the new genes. Specific uses are described for each of the  
CC 52 genes, based on the tissues in which they are most highly expressed,  
CC and include developing products for the diagnosis or treatment of  
CC proliferative disorders, cancer, tumours, foetal and developmental  
CC abnormalities, haematopoietic disorders, diseases of the immune system,  
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
CC allergies, neurological disorders (e.g., Alzheimer's disease,  
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
CC disorders, and infections. The proteins can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues, to identify their  
CC cognate ligands or binding partners, and in chemotaxis, and can be used  
CC as a food additive or preservative to modify storage properties.  
CC Antibodies specific for a protein of the invention can be used in  
CC alleviating symptoms associated with the disorders mentioned above, and  
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
CC immunosorbent assay (ELISA). The present sequence represents a human  
CC secreted protein of the invention.  
XX  
SQ Sequence 316 AA:  
  
Query Match 15.2%; Score 239; DB 22; Length 316;  
Best Local Similarity 27.5%; Pred. No. 3.1e-13;  
Matches 71; Conservative 46; Mismatches 109; Indels 32; Gaps 9;  
QY 20 IRWESPAMASLGQILFMSIISIIILLAGATLIIIGFGSGRHSITVTVASAGNIGEDG 79  
Db 2 IIRYSPGPMG-----VHVGAAIGALWfcltgalevqvpdpvalvgtda 46  
QY 80 ILSCYF--EPDIKLSDIYIQLWKEGVGLVHFEKGEKDELSEQDEMFGRFAVFAQYIV 137  
Db 47 tlccsfspgfsiaqlnlwqldtkqlvhsfaegqd---qgsaayanrtalfpdliaq 102  
QY 138 GNASRLKNNVQLTDAGTKYCYITTSKKGANLEKKTGA-FSMPEVNDYN----ASSE 191  
Db 103 gnasrlrlkvrvadegsfctf-vslrldfgsaavslqvaapykspsmtlepnkdlrpgdtv 161  
QY 192 TLRCFAPRMFPQPTVYVMAISOVDGAFSEVSTSELSNSENTMKNVSVLVNT-INNMY 250  
Db 162 tlccssygygypaeavfw--qdgqgvyplcgnvlt-s-qmanegldfvhsillrvlgangty 218  
QY 251 SCMIENDIAKATGDIKVT 268  
Db 219 sclvrnpvlgqdahsavt 236

RESULT 13  
AAB87249  
ID AAB87249 standard; Protein: 534 AA.  
XX  
AC AAB87249;  
XX  
DT 27-MAR-2001 (first entry)

XX  
DE Human amyloid precursor protein protease SEQ ID NO: 2.  
XX  
KW Human: amyloid precursor protein protease; Alzheimer's disease;  
KW neurodegenerative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200068266-A1.  
XX  
PD 16-NOV-2000.  
XX  
PF 09-MAY-2000; 2000WO-US06707.  
XX  
PR 11-MAY-1999; 99US-0133423.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Becker GW, Hale JE, Heath WF, Johnstone EM, Little SP, Tu Y;  
PI Yeh W, Yin T;  
XX  
DR MPI: 2001-016080/02.  
XX  
N-PSDB: AAC66921.  
XX  
PT New amyloid precursor protein proteases and nucleic acids useful for  
PT identifying amyloid precursor protein protease inhibitors for treating  
PT or preventing Alzheimer's disease and other neurodegenerative diseases  
-  
XX  
PS Claim 1; Page 4-6; 82pp; English.  
XX  
CC The present sequence is a human amyloid precursor protease protein.  
CC Amyloid precursor protein builds up in the brain of individuals with  
CC Alzheimer's disease, and the sequences of the invention can be used to  
CC identify compounds which can be used to prevent and treat the disease. In  
CC addition, they are suitable for use in the treatment of other  
CC neurodegenerative diseases. Down's syndrome and hereditary cerebral  
CC haemorrhage with amyloidosis of the Dutch-type (HCHWA-D).  
XX  
SQ Sequence 534 AA:  
  
Query Match 15.2%; Score 239; DB 22; Length 534;  
Best Local Similarity 27.5%; Pred. No. 6.3e-13;  
Matches 71; Conservative 46; Mismatches 109; Indels 32; Gaps 9;  
QY 20 IRWESPAMASLGQILFMSIISIIILLAGATLIIIGFGSGRHSITVTVASAGNIGEDG 79  
Db 2 IIRYSPGPMG-----VHVGAAIGALWfcltgalevqvpdpvalvgtda 46  
QY 80 ILSCYF--EPDIKLSDIYIQLWKEGVGLVHFEKGEKDELSEQDEMFGRFAVFAQYIV 137  
Db 47 tlccsfspgfsiaqlnlwqldtkqlvhsfaegqd---qgsaayanrtalfpdliaq 102  
QY 138 GNASRLKNNVQLTDAGTKYCYITTSKKGANLEKKTGA-FSMPEVNDYN----ASSE 191  
Db 103 gnasrlrlkvrvadegsfctf-vslrldfgsaavslqvaapykspsmtlepnkdlrpgdtv 161  
QY 192 TLRCFAPRMFPQPTVYVMAISOVDGAFSEVSTSELSNSENTMKNVSVLVNT-INNMY 250  
Db 162 tlccssygygypaeavfw--qdgqgvyplcgnvlt-s-qmanegldfvhsillrvlgangty 218  
QY 251 SCMIENDIAKATGDIKVT 268  
Db 219 sclvrnpvlgqdahsavt 236

RESULT 14  
AAB87417  
ID AAB87417 standard; Protein: 216 AA.  
XX  
AC AAB87417;  
XX







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